

RA Haged F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,  
RA Woodbury R.G., Hart C.E., Insley M.Y., Kisiel W., Kurachi K.,  
RA Davi G.W.,  
RT "Characterization of a cDNA coding for human factor VII.",  
RL Proc Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=87260948; PubMed=3037537;  
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,  
RA Haged F.S., Murray M.J.;  
RT "Nucleotide sequence of the gene coding for human factor VII, a  
RT vitamin K-dependent protein participating in blood coagulation.",  
RL Proc Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
RN [3]  
RN SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.  
RA Riedel M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  
RP MEDLINE=89088153; PubMed=3264725;  
RA Thim L., Bloern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,  
RA Pedersen A.H., Hedner U.;  
RT "Amino acid sequence and posttranslational modifications of human  
RT factor VIIa from plasma and transfected baby hamster kidney cells.",  
RL Biochemistry 27:7785-7793(1988).  
RN [5]  
RN CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
RP MEDLINE=91250411; PubMed=1904059;  
RA Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,  
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.,  
RA Shimomishi Y., Iwanaga S.;  
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
RT (Xyl-Glc) O-glycosidically linked to a serine residue in the first  
RT epidermal growth factor-like domain of human factors VII and IX and  
RT protein Z and bovine protein Z.",  
RL J. Biol. Chem. 266:11051-11057(1991).  
RN [6]  
RN STRUCTURE OF CARBOHYDRATE ON SER-112.  
RP MEDLINE=9062160; PubMed=2511201;  
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.,  
RA Shimomishi Y., Iwanaga S.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the  
RT first EGF-like domain of clotting factors VII and IX and protein Z.",  
RL Adv. Exp. Med. Biol. 281:121-131(1990).  
RN [8]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TP.  
RP MEDLINE=96175641; PubMed=8598903;  
RA Banerji D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
RT "The crystal structure of the complex of blood coagulation factor  
RT VIIa with soluble tissue factor.",  
RL Nature 380:41-46(1996).  
RN [9]  
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TP.  
RP MEDLINE=99126538; PubMed=9925787;  
RA Zhan E., St Charles R., Tulinsky A.;  
RT "Structure of extracellular tissue factor complexed with factor VIIa  
RT inhibited with a BPTI mutant.",  
RL J. Mol. Biol. 285:2089-2104(1999).  
RN [10]  
RN STRUCTURE BY NMR OF 105-145.  
RP MEDLINE=98367502; PubMed=9692950;  
RA Murayama A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,  
RA Drakenberg T.;  
RT "Solution structure of the N-terminal EGF-like domain from human

RT factor VII.",  
RL Biochemistry 37:10605-10615(1998).  
RN [11]  
RN VARIANT GLN-364.  
RX MEDLINE=91300046; PubMed=2070047;  
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
RA Meade T.W., Tuddenham E.G.D.;  
RT "Purification and characterization of factor VII 304-Gln: a variant  
RT molecule with reduced activity isolated from a clinically unaffected  
RT male.",  
RL Blood 78:132-140(1991).  
RN [12]  
RN VARIANTS GLN-364 AND PHE-370.  
RP MEDLINE=92340074; PubMed=1634227;  
RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,  
RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;  
RT "Detection of two missense mutations and characterization of a repeat  
RT polymorphism in the factor VII gene (F7).",  
RL Hum. Genet. 89:497-502(1992).  
RN [13]  
RN VARIANT TYR-238.  
RP MEDLINE=93372811; PubMed=8364544;  
RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.;  
RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms  
RT (115His and 333Ser) in the human coagulation factor VII gene.",  
RL Hum. Mol. Genet. 2:1055-1056(1993).  
RN [14]  
RN VARIANTS  
RP MEDLINE=94061028; PubMed=8242057;  
RA Takamiya O., Kambali-Cook G., Martin D.M.A., Cooper D.N.,  
RA von Felten E., Meili E., Hahn I., Prangnell D.R., Lumley H.,  
RA Tuddenham E.G.D., McVey J.H.;  
RT "Detection of missense mutations by single-strand conformational  
RT polymorphism (SSCP) analysis in five dysfunctional variants of  
RT coagulation factor VII.",  
RL Hum. Mol. Genet. 2:1355-1359(1993).  
RN [15]  
RN VARIANTS CHARLOTTE GLN-139 AND GLN-212.  
RX MEDLINE=94264305; PubMed=8204879;  
RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,  
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
RT "Severe factor VII deficiency caused by mutations abolishing the  
RT cleavage site for activation and altering binding to tissue factor.",  
RL Blood 83:3524-3535(1994).  
RN [16]  
RN VARIANT VAL-354.  
RP MEDLINE=95072589; PubMed=7981691;  
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,  
RA Rodeghiero F., Marchetti G.;  
RT "Topologically equivalent mutations causing dysfunctional coagulation  
RT factors VII (294Ala->Val) and X (334Ser->Pro).",  
RL Hum. Mol. Genet. 3:1175-1177(1994).  
RN [17]  
RN VARIANT MIE HIS-307.  
RX MEDLINE=95064662; PubMed=7974346;  
RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,  
RA Suzuki K.;  
RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by  
RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
RT catalytic domain.",  
RL Thromb. Haemost. 71:773-777(1994).  
RN [18]  
RN VARIANT MET-419.  
RX MEDLINE=96247510; PubMed=8652821;  
RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
RT "A Thr359Met mutation in factor VII of a patient with a hereditary  
RT deficiency causes defective secretion of the molecule.",  
RL Blood 87:5085-5094(1996).  
RN [19]  
RN VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.  
RX MEDLINE=97001216; PubMed=8844208;  
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,  
RA Lunghi B., Rodeghiero F., Marchetti G.;



DR SMART: SM00179; EGF\_CA: 1.  
 DR SMART: SM00069; GLA: 1.  
 DR SMART: SM00020; TRYP\_SPC: 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL: 1.  
 DR PROSITE: PS00022; EGF\_1: 1.  
 DR PROSITE: PS00186; EGF\_2; FALSE\_NEG.  
 DR PROSITE: PS00187; EGF\_CA: 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION: 1.  
 DR PROSITE: PS00240; TRYP\_SIN\_DOM: 1.  
 DR PROSITE: PS00134; TRYP\_SIN\_HIS: 1.  
 DR PROSITE: PS00135; TRYP\_SIN\_SER: 1.  
 KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KW EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT PROPEP 25 41 POTENTIAL.  
 FT CHAIN 42 193 FACTOR VII LIGHT CHAIN.  
 FT CHAIN 194 446 FACTOR VII HEAVY CHAIN.  
 FT DOMAIN 47 76 GLA-RICH.  
 FT DOMAIN 87 123 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 128 169 EGF-LIKE 2.  
 FT DOMAIN 194 446 SERINE PROTEASE.  
 FT SITE 193 194 CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN) (BY SIMILARITY).  
 FT ACT\_SITE 234 234 BY SIMILARITY.  
 FT ACT\_SITE 283 283 BY SIMILARITY.  
 FT ACT\_SITE 385 385 BY SIMILARITY.  
 FT BINDING 379 379 SUBSTRATE (BY SIMILARITY).  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT DISULFID 96 111 BY SIMILARITY.  
 FT DISULFID 113 122 BY SIMILARITY.  
 FT DISULFID 132 143 BY SIMILARITY.  
 FT DISULFID 139 153 BY SIMILARITY.  
 FT DISULFID 155 168 BY SIMILARITY.  
 FT DISULFID 176 303 BY SIMILARITY.  
 FT DISULFID 200 205 BY SIMILARITY.  
 FT DISULFID 219 235 BY SIMILARITY.  
 FT DISULFID 351 370 BY SIMILARITY.  
 FT DISULFID 381 409 BY SIMILARITY.  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 104 104 HYDROXYLATION (BY SIMILARITY).  
 FT CARBHYD 186 186 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBHYD 244 244 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 446 AA; 50276 MW; 2512644A45CBC96E CRC64;

Query Match 34.5%; Score 909.5; DB 1; Length 446;  
 Best Local Similarity 39.08; Pred. No. 1e-58;  
 Matches 187; Conservative 77; Mismatches 140; Indels 75; Gaps 10;

QY 16 GLLL-----LGSLFIRBQANNILARVTRANSFLEMKKGLHREMEETCSYE 65  
 DQ 7 GLLLCFLQLQGLPLGAVFTQBEAHGVLHRRANSLLLELWPGSLERECEQCSFE 66  
 QY 66 EAREVFEDSKTNEFWNKYKDGDCETSPCQNOGCKDKGLGEYCTCTCLEGFEKGNELFT 125  
 DQ 67 EAREIFKSPRTKQFWIVSDQACASPCQNGGTQCDHLKSYVCFCLLDFEGRNCEKSK 126  
 QY 126 RK--LCSLDNGDCDFCHEEQNSV--VCSCARGYTLADNGKACIPGYPGCK-QTLERRK 181  
 DQ 127 NEQLICANENGDCDQYCRDHVGTKRTCSCHEDYTLQPDVEVSCPKYPCGRIPVVEKRN 186  
 QY 182 RSVAQATSSSGEAPSDSTWPKPYDAADLDPTENPFDLLDFNQTOPERGDNNLRTIVGGQEC 241

DB 187 SSSROG-----FCGCTILSEFVILTAACHLYQAK---RFGVVRGDRNTEQ 295  
 QY 242 KDGECPWOALL-INEENEG--FCGCTILSEFVILTAACHLYQAK---RFGVVRGDRNTEQ 295  
 DB 201 PKGECPMQAVLKIN---GLLCGAVLLDARWIVTAACHFNIRVWGNITVVMGHDSE 256  
 QY 296 EEGEAVHEVEVVIKHNRTKTYDFDIARLRLKTPITFRMNVAPACLPDRWAESTLMT 355  
 DB 257 KDGEQRRVTVQVIMPKYIRKINHDIALLRLHRPVFTDYVVPCLCLPEKSFSENTLAR 316  
 QY 356 QKTGVISGFRTHRGROSTRKLMLEVPYVDRNSC-----KLSSFIITQMFACGYDTK 410  
 DB 317 IRFSVSGWQLDRGATALEMSIEVPLMTQDCLEHAHKSSTPKITENMFCAGYMDG 376  
 QY 411 QEDACQDGGGPHVTREKDYTVGTGIVSGWGESCARCKYGIYKVTAFKLWIDRSMKTR 469  
 DB 377 TKDACKDGGGPHATHYHGTWLTGTVSGEGCAAIGHIVTVRSQIDMLVRHMSK 435

RESULT 13  
 FA7\_BOVIN STANDARD; PRT; 407 AA.  
 ID P22457;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
 DE F7.  
 GN F7.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP MEDLINE=89008362; PubMed=3049594;  
 RX Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,  
 RA Iwanaga S.;  
 RT "Bovine factor VII. Its purification and complete amino acid  
 RT sequence.";  
 RL J. Biol. Chem. 263:14868-14877(1988).  
 [2]  
 RN STRUCTURE OF CARBOHYDRATE ON SER-52.  
 RX MEDLINE=89213999; PubMed=3149637;  
 RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,  
 RA Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT blood coagulation factors VII and IX.";  
 RL J. Biochem. 104:867-868(1988).  
 RN [3]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein 2.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 11.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.

DR PIR; A31979; KEB07.  
 DR HSP; P06709; IBF9.  
 DR MEROS; S01.215; -.  
 DR IntePro; IPR000152; Asx\_hydroxyl.  
 DR IntePro; IPR001314; Chymotrypsin.  
 DR IntePro; IPR000742; EGF\_2.  
 DR IntePro; IPR001881; EGF\_Ca.  
 DR IntePro; IPR001438; EGF\_II.  
 DR IntePro; IPR006209; EGF\_like.  
 DR IntePro; IPR002383; GLA\_blood.  
 DR IntePro; IPR001254; Ser\_protease\_Try.  
 DR IntePro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00010; EGF\_blood.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS001187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPsin\_DOM; 1.  
 DR PROSITE; PS00134; TRYPsin\_SER; 1.  
 DR PROSITE; PS00135; TRYPsin\_HIS; 1.  
 DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KW EGF-like domain; Repeat.  
 FT CHAIN 1 152  
 FT CHAIN 153 407  
 FT DOMAIN 6 35  
 FT DOMAIN 46 82  
 FT DOMAIN 87 128  
 FT DOMAIN 153 407  
 FT SITE 152 153  
 FT ACT\_SITE 193  
 FT ACT\_SITE 242  
 FT ACT\_SITE 344  
 FT BINDING 338  
 FT DISULFID 17 22  
 FT DISULFID 50 61  
 FT DISULFID 55 70  
 FT DISULFID 72 81  
 FT DISULFID 91 102  
 FT DISULFID 98 112  
 FT DISULFID 114 127  
 FT DISULFID 135 262  
 FT DISULFID 159 164  
 FT DISULFID 178 194  
 FT DISULFID 310 329  
 FT DISULFID 340 368  
 FT MOD\_RES 6  
 FT MOD\_RES 7  
 FT MOD\_RES 14 14  
 FT MOD\_RES 16 16  
 FT MOD\_RES 19 19  
 FT MOD\_RES 20 20  
 FT MOD\_RES 25 25  
 FT MOD\_RES 26 26  
 FT MOD\_RES 29 29  
 FT MOD\_RES 35 35  
 FT MOD\_RES 52 52  
 FT CARBOHYD 145  
 FT CARBOHYD 203  
 FT CARBOHYD 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;  
 Query Match 33.1%; Score 872; DB 1; Length 407;  
 Best Local Similarity 38.7%; Pred. No. 4.7e-56;

Matches 174; Conservative 71; Mismatches 137; Indels 68; Gaps 9;  
 QY 41 ANSLEEMKKGHLRECEMEETCSYEAREVFEQSDKTFNFWKYKDGQDCQCTSPCONQK 100  
 DB 1 ANGFELELLPGSLERECEELCSFEAEHFRNEERTRQFWVSYNDGDCQACSSPCQNGS 60  
 QY 101 CKDGLGYTCTCLEGFEKNCCL--FTRKLCSLDNGDCQFCHEEQNS--VVCSCARGYTL 157  
 DB 61 CEDQLRSYICFCPDGFEGRNCETDKQSOLICANDNGGCEQYCGADPGAGRFCWCHEGYAL 120  
 QY 158 ADNGKACIPTGPPCGK-QTLERKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFD 216  
 DB 121 QADGVCAPIVEYPCGKIPVLEKRNKSKPQG----- 151  
 QY 217 LLDFNOTQPERGDNLTIRIVGGQCKDGECPQWALLINEENEGFCGGTILSEFYILTAAH 276  
 DB 152 -----RIVGGHVCPEKGECPQWAML-KLNGALLCGTLVGPWWVSAAH 193  
 QY 277 CLYQAKREFKVR-----VGRNTEQEGGGAHVHEVVEVIKHNRTKTYDFDIARLKT 330  
 DB 194 CF---ERLSRGNLTAVLGEHDLRSVEGPEQERRVAQIIIVPKQYVPGQTDHVDALLQLAQ 250  
 QY 331 PITFRMNVAPACLPERDWAESTLMTOKTGVSGFGRTHKRGROSTRKMLLEVYPVDNRSC 390  
 DB 251 PVALGDHVAFLCLPDPDFADQTLAFVRFSAVSGWQLLERGVTAARKLMVVLVPRLLTQDC 310  
 QY 391 KLSS-----SFIITQNMFCAGYDTKQEDACQSGGPHVTRFKDTYFTVTGIVSWGSCAR 445  
 DB 311 LQOSRQRPQGPVVDNMFACAGSDGSKDACKDGGPHATFRGTFRGTWLTGWSWGEGCAA 370  
 QY 446 KGXYGIYTKYTAFLKWDNRKMRGLPKAK 475  
 DB 371 AGHFGIYTRVSRYTAWLRQLM---GHPPSR 397  
 RESULT 14  
 PRTC\_BOVIN  
 ID PRTC\_BOVIN STANDARD; PRT; 456 AA.  
 AC P00745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=85014826; PubMed=6091100;  
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.;  
 FT "Cloning and sequencing of liver cDNA coding for bovine protein C.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
 RN [2]  
 RN SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.  
 RX MEDLINE=83007325; PubMed=6896876;  
 RA Fernlund P., Stenflo J.;  
 FT "Amino acid sequence of the light chain of bovine protein C";  
 RL J. Biol. Chem. 257:12170-12179(1982).  
 RN [3]  
 RN REVISION TO 110.  
 RX MEDLINE=83169769; PubMed=6572939;  
 RA Drakenberg T., Fernlund P., Koepstorff P., Stenflo J.;  
 FT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
 RN [4]  
 RN SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350  
 AND ASN-366.  
 RX MEDLINE=83007326; PubMed=6896877;



RA Sterio J., Fernlund P.;  
 RT "Amino acid sequence of the heavy chain of bovine protein C.";  
 RL J. Biol. Chem. 257:12180-12190(1982).  
 RN [5]  
 RP PROTEIN BINDING AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213513; PubMed=6304092;  
 RA Esmon N.L.; Debault L.E., Esmon C.T.;  
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-  
 domainless protein C.";  
 RL J. Biol. Chem. 258:5548-5553(1983).  
 RN [6]  
 RP PROTEIN BINDING AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213514; PubMed=6406503;  
 RA Johnson A.E., Esmon N.L., Iau T.M., Esmon C.T.;  
 RT "Structural changes required for activation of protein C are induced  
 by Ca<sup>2+</sup> binding to a high affinity site that does not contain gamma-  
 carboxyglutamic acid.";  
 RL J. Biol. Chem. 258:5554-5560(1983).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC -1- IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- ISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- TISSUE: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL K02435; AAA30685.1; -  
 DR PIR: A26250; KXBO.  
 DR HSP: P04070; LPCU.  
 DR MEROPS: S01.218; -  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR006209; EGF-like.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR001254; Ser.protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam PF00008; EGF; 2.  
 DR Pfam PF00594; gla; 1.  
 DR Pfam PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00181; EGF; 2.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; Tryp\_Spc; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.

DR PROSITE: PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 29  
 FT PROPEP 30 39  
 FT CHAIN 40 194  
 FT CHAIN 197 456  
 FT PEPTIDE 197 210  
 FT DOMAIN 94 129  
 FT DOMAIN 133 173  
 FT DOMAIN 211 456  
 FT MOD\_RES 45 45  
 FT MOD\_RES 46 46  
 FT MOD\_RES 53 53  
 FT MOD\_RES 55 55  
 FT MOD\_RES 58 58  
 FT MOD\_RES 59 59  
 FT MOD\_RES 62 62  
 FT MOD\_RES 64 64  
 FT MOD\_RES 65 65  
 FT MOD\_RES 68 68  
 FT MOD\_RES 74 74  
 FT MOD\_RES 110 110  
 FT ACT\_SITE 252 252  
 FT ACT\_SITE 298 298  
 FT ACT\_SITE 397 397  
 FT DISULFID 56 61  
 FT DISULFID 89 108  
 FT DISULFID 98 103  
 FT DISULFID 102 117  
 FT DISULFID 119 128  
 FT DISULFID 137 148  
 FT DISULFID 144 157  
 FT DISULFID 159 172  
 FT DISULFID 180 318  
 FT DISULFID 237 253  
 FT DISULFID 368 382  
 FT DISULFID 393 421  
 FT CARBOHYD 136 136  
 FT CARBOHYD 289 289  
 FT CARBOHYD 350 350  
 FT CARBOHYD 366 366  
 FT VARIANT 82 82  
 FT CONFLICT 455 456  
 SQ SEQUENCE 456 AA; 51407 MW; CAAF6833F894C209 CRC64;  
 Query Match 33.1%; Score 872; DB 1; Length 456;  
 Best Local Similarity 38.7%; Pred. No. 5,4e-56;  
 Matches 183; Conservative 83; Mismatches 155; Indels 52; Gaps 10;  
 QY 22 ESLFTRRQANNILARVTRANSFLBEMKKHLEECMEETCSYBEAREVFDSDKTNFEW 81  
 DB 21 DSVFSSQRAHQVLRIRKRRANSFLBRLPGNVERSECEVEFEAREIFQNTDPAF 80  
 QY 82 NKYKGDQCEYS-----PCONOGCKDGGLGEVTCFLEGFEKNCLEFTR-KLCSLD 132  
 DB 81 SFYSDGQCEDEPRSPGCDLPCCGRGKCIDGLGGFCDCAGWEGFCLHEVRFNSCSAE 140  
 QY 133 NGDCDQFCHEEQNSVVCARGYTLADNGKACIPTPGPGK--OTLERRKRSVAQATSS 190  
 DB 141 NGGCAHYCMEEBRRHRCSCAPGYRLEDHQLCVSKVTPFCGRGLGRMEKRRKTLKRDNTQ 200  
 QY 191 SCEAPDSITWKPYDAAD-LDPTENPFDLLDFNQTPERGDNLLTRIVGQCKGCECPWQ 249  
 DB 201 -----VDQKDQLDP-----RIVDQAGWGESPMQ 225  
 QY 250 ALLINEEGFCGGTILSEFYILTAAHCLYQAKRFKVRGDRNTQEGEGGAVHEVEVVI 309  
 DB 226 AVLLDSKKLVGCGAVLIHVSVLTVARCLDSKKLIIVLGEYDMRRNESWEDLDIKEVI 285

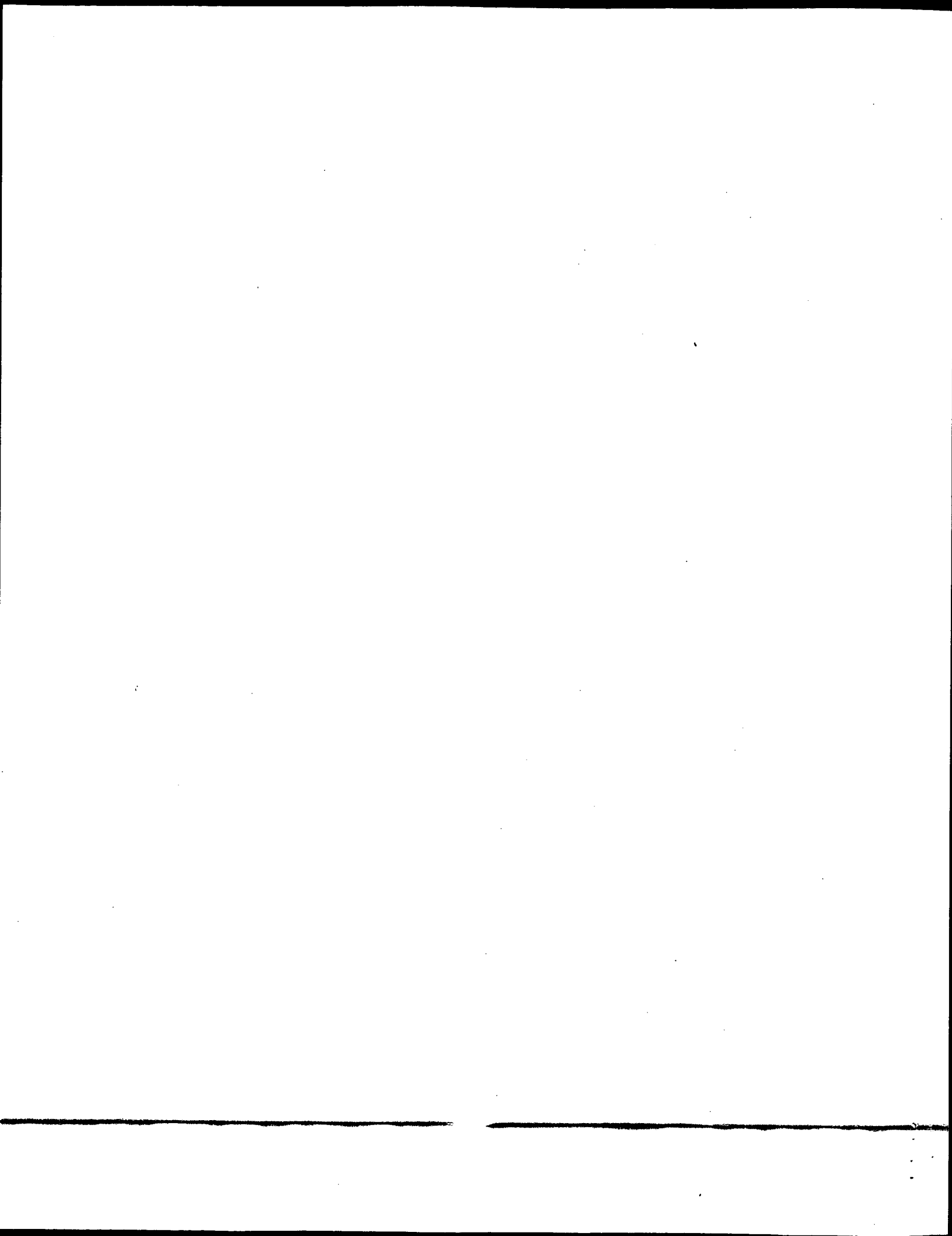
QY 310 KHNFTKTYDEDFIARLRLKTPITFRMNVAPACLPDRWAES--TLMQTKTGVISGFGRT 367  
 Db 286 IHPNFKSTSDNDIALRLAKPATLSQTIVPICLPDGLSERKLTQVGOET-VVTGWYR 344  
 QY 368 HEKRGQST-RLKMLEVFPYVDRNSCKLSSPFIITONMFCAGYDFKQEDACQDGGSGPHVTR 426  
 Db 345 DETKRNFTFVLSIKFVVPVYNACVIAEMNKISENMLCAGILGDPDRDCEGSGGPMVTF 404  
 QY 427 FKDTYFVTGVSGECARKGKYGIYTKVTAFLKWLIDRSMKTRGLPKAKSHAP 479  
 Db 405 FRGTWFLVGLVSGEGGRLYNGVTVKVSRYLDWLYGHKIAQEA-LESQVP 456

RESULT 15  
 PRTC\_RAT STANDARD; PRT; 461 AA.  
 AC P31394;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 24, Last annotation update)  
 DE Vitamin-K-dependent protein C precursor [EC 3.4.21.69]  
 DE (Antithrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).  
 DE PROCC  
 GN Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAN-Wistar; Tissue-Liver;  
 RX MEDLINE=92329550; PubMed=1627650;  
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;  
 RL "The cDNA cloning and mRNA expression of rat protein C.";  
 CC Biochim. Biophys. Acta 1131:329-332(1992).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- ISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- TM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL X64336; CAA45617.1; -;  
 DR PIR S18994; S18994.  
 DR HSSP P04070; LPCU.  
 DR MEROPS S01.218; -;  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001881; EGF\_CA.  
 DR InterPro: IPR006209; EGF\_like.  
 DR InterPro: IPR002383; GLA\_blood.

DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF; 2.  
 DR Pfam: PF00594; gla; 1.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PRO0722; CHYMOTRYPSIN.  
 DR PRINTS: PRO0001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; TRYPSIN\_SPC; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxylglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 FT SIGNAL 1 32  
 FT PROPEP 33 41  
 FT CHAIN 42 196  
 FT PEPTIDE 199 461  
 FT SITE 212 213  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 213 461  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 112 112  
 FT ACT\_SITE 254 254  
 FT ACT\_SITE 300 300  
 FT ACT\_SITE 402 402  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
 FT DISULFID 104 119  
 FT DISULFID 121 130  
 FT DISULFID 139 150  
 FT DISULFID 146 159  
 FT DISULFID 161 174  
 FT DISULFID 182 320  
 FT DISULFID 239 255  
 FT DISULFID 373 387  
 FT DISULFID 398 426  
 FT CARBOHYD 291 291  
 FT CARBOHYD 355 355  
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;

Query Match 32.7%; Score 861; DB 1; Length 461;  
 Best Local Similarity 36.4%; Pred. No. 3.4e-55;  
 Matches 182; Conservative 81; Mismatches 159; Indels 78; Gaps 11;





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2003, 10:23:44 ; Search time 103 seconds  
(without alignments)  
1222.618 Million cell updates/sec

Title: US-09-632-722-2  
Perfect score: 2634  
Sequence: 1 MGRLHLVLSASLAGLLLL.....RGLPKAKSHAPEVITSSPLK 488

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_Organelle:\*
- 9: sp\_Phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirm:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Prep. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193.5	75.7	481	11	O88947 mus musculus
2	192.5	75.6	481	11	Q99132 mus musculus
3	190.5	75.6	481	11	O54740 mus musculus
4	1957	74.3	482	11	Q63207 rattus norv
5	106.5	64.8	469	6	Q96MD9
6	114.5	42.3	376	13	P83370
7	1101	41.8	474	13	O8JHC8
8	139.5	39.5	456	4	Q14316
9	138.5	39.4	461	6	Q95ND7
10	103.5	38.1	461	6	Q95ND6
11	946	35.9	701	4	Q96EQ8
12	36.5	35.6	433	13	Q90YK1
13	35.5	35.5	433	13	O8JHD0
14	932	35.4	503	13	O8AYE4
15	90.5	34.5	446	11	Q61109
16	904.5	34.3	446	11	Q8K3U6 rattus norv

Q9ttro canis famil  
Q9lwn8 mus musculu  
Q99pc6 mus musculu  
Q8jhc9 brachydanio  
Q28511 macaca mula  
Q60546 mesocricetu  
Q63109 rattus norv  
Q77669 canis famil  
Q9ptw7 struthio ca  
Q91001 gallus gall  
Q9cqw3 mus musculu  
Q8ci01 mus musculu  
Q967x8 panulirus a  
Q90504 eptaretus  
Q91004 gekko gekko  
Q8aggr2 xenopus lae  
Q9db10 mus musculu  
Q81925 hyphantria  
Q91674 xenopus lae  
Q9cpn7 mus musculu  
Q14520 homo sapien  
Q9vdu8 drosophila  
Q81ue2 homo sapien  
Q81u80 homo sapien  
Q81927 hyphantria  
Q28994 sus scrofa  
Q91vp2 mus musculu  
Q8bye2 homo sapien  
Q17039 anopheles g

#### ALIGNMENTS

#### RESULT 1

O88947 PRELIMINARY; PRT; 481 AA.  
ID AC O88947;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Coagulation factor X precursor.  
GN F10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL6 X CBA; TISSUE=Liver;  
RX MEDLINE=98347933; PubMed=9684791;  
RA Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,  
RA Castellino F.J., Rosen E.D.;  
RT "Cloning and characterization of a cDNA encoding murine coagulation  
RT factor X";  
RL Thromb. Haemost. 80:87-91(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129Sj;  
RA Cooper A., Liang Z., Castellino F.J., Rosen E.D.;  
RT "Cloning and Characterization of the Murine Factor X Gene.";  
RL Thromb. Haemost. 0:0-0(2000).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL: AF087644; AAC36345.1; -;  
DR EMBL: AF211347; AAF22980.1; -;  
DR HSSP: P00742; 1XKA.  
DR MEROPS: S01.216; -;  
DR MGD: MGI:103107; F10.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR001438; EGF\_II.



```

QY 420 GPHVTRFKDITVTVTVGIVSWGSCARKGYIYTKVTAFLKWDIDSMKTRGLPKAKS 476
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 417 GPHVTRFKNTYYTVTVGIVSWGECARKGYIYTKVTTTLKWDIDSMKARVGPATAET 473

RESULT 3
OS4740 ID 054710 PRELIMINARY; PRT; 481 AA.
AC 054710;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 DR FAL0.
OS Mus musculus (Mouse).
OC plasmid pBluescript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98454993; PubMed=9783672;
RA Heidmann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL AJ222677; CAA10933.1; -.
DR HSSP P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam PF00008; EGF; 2.
DR Pfam PF00594; gla; 1.
DR Pfam PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease; Signal;
KW plasmid.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 481 AA; 53986 MW; CF702DE5EF9D7AE CRG64;

Query Match 75.6%; Score 1990.5; DB 11; Length 481;
Best Local Similarity 76.3%; Pred. No. 7.1e-186;
Matches 364; Conservative 45; Mismatches 63; Indels 5; Gaps 2;

QY 1 MGRPLHLVLLSLAGLLGLSLFIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSVPQLSLCVVLSLLPGKGVFINRANVLARTANSFFEFKKNLERECMEE 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 TCSYEAREVFEDSKTNFVWYKDGQCETSPQNGCKKDLGLEYTCTCLEGFEKGN 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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Db 61 ICSYEEVREIFEDEKTEYWTYKYGDCQCESSPCQNGACRDGIGGYTCTCSEGFEGKN 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 CELFTRKLCSDNGDCQDFCHEEONSVCVSCARGYTLADNGKACIPGYPYCGKQTLERR 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 CELFVRKLCRLDNGDCQDFCHEEONSVCVSCARGYTLADNGKACISAPFPYCGKITGRR 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 KRSVAQATSSSG-EAPDSITWKPYDAADLPDPTNPFDLLDFNQTPERGDNMLTRYVGGQ 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KRSVALNTSDSELDLEDALEAL---LDEDFLSTPENIELNLNETQPERSSDDLVRYVGR 236
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 ECKDGECPWQALLNEENEGFCGGTILSEFYLTAACHLYQAKRFKRVGDRNTEQEGG 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 ECKDGECPWQALLNEENEGFCGGTILNEFYLTAAHCLHQAARFKRVGDRNTEKEDGN 296
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 EAVHEVEVVIKHNRTKETDYDIAVLRLKPTIFRMNVAPACLPERDWAESTLMTOKTG 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 ELVHEVDVVVINKNFQROTIDYIAVLRLKPTIFRMNVAPACLPQDWAESTLMTOKTG 356
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 IVSGFGRTHKGRQSTRLMLEVPYVDRNSCKLSSEFIIQNMFCAGYDTYKQEDACQGDS 419
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 357 IVSGFGRTHKGRQSNILKMLEVPYVDRNTCKLSFSEITQNMFCAGYEAKLEDACQGDS 416
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 GPHVTRFKDITVTVTVGIVSWGSCARKGYIYTKVTAFLKWDIDSMKTRGLPKAKS 476
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 417 GPHVTRFKNTYYTVTVGIVSWGECARKGYIYTKVTTTLKWDIDSMKARVGPATAET 473
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
Q63207 ID Q63207 PRELIMINARY; PRT; 482 AA.
AC Q63207;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
    for intracellular processing by the vitamin K-dependent gamma-
    carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; X79807; CAA56202.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 2.

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DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match
Best Local Similarity 74.3%; Score 1957; DB 11; Length 482;
Matches 359; Conservative 54; Mismatches 63; Indels 8; Gaps 3;

QY 1 MGRPLHLVLLSASLGLLLGESLFIHQANILARVTRANSFLEEMKKGHLERECME 60
Db 1 MESVRLSLVLLVSLPGLRSPVFINRERANNVLRIRANSFEEIKKGNLERECVEE 60
QY 61 TCSYEAREVEFSDSKTNEFWNKYKDGDCQSPCONQCKGKGLGVTCTCLEGFEKN 120
Db 61 ICSFEAREVEFDEKTEFWNKYKDGDCQSPCONQCKGKGLGVTCTCTEGFEKN 120
QY 121 CELFTKRLCSLDNGDCQFCHEQNSVVCARGYTLDNGKACIPTGYPGCKQTLERR 180
Db 121 CELFVRKLCSLDNGDCQFCHEQNSVVCARGYTLDNGKACIPTGYPGCKQTLERR 180
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENFDLLDFNQTOPERCDDNLTFRVGOE 240
Db 181 KRSVALNTSNSEPPEDLM---PDADILYPTESPSELLNLTKEPEANSDDVIRVGGQE 237
QY 241 CKDGECPQWALLI-NEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGRDNTPEQEGG 299
Db 238 CKRGECPQWALLFSDDETDGCGGTILNEFYILTAACHLYQAKRFKRVGRDNTPEQEGG 297
QY 300 EAVHEVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAPACLPEDRWAESTLMTQKTG 359
Db 298 EMVHEVDVIKHNKRFQDITYDFDIAVLRLKTPITFRMNVAPACLPQKDWAEATLMTQKTG 357
QY 360 IVSGFGRTHKGRQSTRKLMLEVPYVDNRNSKLSSTFIQNMFCAGYDTKQEDACOGDS 419
Db 358 IVSGFGRTHKGRQSKVLKMEVPYVDNRNTCLSTFSITQNMFCAGYDTKQEDACOGDS 417
QY 420 GPHVTREKDYFYFTGIVSWGECARGKYGIYTKVTAFLKWIIDRSMTKRLPKAK--- 475
Db 418 GPHVTREKDYFYFTGIVSWGECARGKYGIYTKVTAFLKWIIDRSMTKRLPKAK--- 477
QY 476 SHAP 479
Db 478 THPP 481

RESULT 5
Q9GMD9 PRELIMINARY; PRT; 469 AA.
ID Q9GMD9;
AC Q9GMD9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Coagulation factor X.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015017; PubMed=11132153;
RA Poorafshar M., Aveskogh M., Munday B., Hellman L.;
RT "Identification and structural analysis of four serine proteases in a
RT monotreme, the platypus, Ornithorhynchus anatinus.";
RL Immunogenetics 52:19-28(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL AF275654; AAG00453.1;
DR HSSP P00742; 1XKB.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx_hydroxyl.

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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match
Best Local Similarity 64.8%; Score 1706.5; DB 6; Length 469;
Matches 314; Conservative 58; Mismatches 90; Indels 11; Gaps 4;

QY 1 MGRPLHLVLLSASLGLLLGESLFIHQANILARVTRANSFLEEMKKGHLERECME 60
Db 1 MAGRLHLVLLFALFSLAPPVENVFINQEDANKVLGRAKRANSLFELAKKGNLERECNEE 60
QY 61 TCSYEAREVEFSDSKTNEFWNKYKDGDCQSPCONQCKGKGLGVTCTCLEGFEKN 120
Db 61 TCSYEAREVEFSDSKTNEFWNKYKDGDCQSPCONQCKGKGLGVTCTCLEGFEKN 120
QY 121 CELFTKRLCSLDNGDCQFCHEQNSVVCARGYTLDNGKACIPTGYPGCKQTLERR 180
Db 121 CDTTTKVICSNLNGDCQFCCKSVVNVVWVSCAQGYTLGDDQKSCIPTPFPCKLTGVR 180
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENFDLLDFNQTQPERGDDNLTFRVGOE 237
Db 181 KRSRELPEODGD-----NAHVAEDVLEATENFEAPDPTTTLAEPGNALVRVIG 233
QY 238 GQECKDGECPWQALLINEEN-EGFCGGTILSEFYILTAACHLYQAKRFKRVGRDNTPEQ 296
Db 234 GRECHDGECPWQALLVNDENGQFCGGTILSEFYILTAACHLYQAKRFKRVGRDNTPEQ 293
QY 297 EGGEAVHEVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAPACLPEDRWAESTLMTQ 356
Db 294 DSSEMAHEVEKVIHVSFKVKTDFDIAVLRLKTPITFRMNVSPACLPEDRWAESTLMTQ 353
QY 357 KTGIVSGFGRTHKGRQSTRKLMLEVPYVDNRNSKLSSTFIQNMFCAGYDTKQEDACQ 416
Db 354 KAGVSGFGRVHEKGRPSVTLKMLEVPYVETTKOSSSFDTIPNMFCAGYDSRPEDACQ 413
QY 417 GDSGGPHVTRFKDITYFTGIVSWGECARGKYGIYTKVTAFLKWIIDRSMTKRL 469
Db 414 GDSGGPHVTRFKDITYFTGIVSWGECARGKYGIYTKVTAFLKWIIDRSMTKRL 466

RESULT 6
P83370 PRELIMINARY; PRT; 376 AA.
ID P83370;
AC P83370;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Coagulation factor X (EC 3.4.21.6) (Hopsarin D).
OS Hoplocephalus stephensi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 Elapidae; Notochordae; Haplocephalus.  
 NCBI TaxID=196418;  
 RN [1]  
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, AND SUBUNIT.  
 KC Tissue-venom gland;  
 RA Rao V.S., Joseph J.S., Kini R.M.;  
 RT "Group D prothrombin activators from snake venom are structural  
 RL homologues of mammalian factor Xa";  
 CC Submitted (MAY-2002) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT  
 CC CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA,  
 CC CALCIUM AND PHOSPHOLIPID DURING BLOOD CLOTTING. ACTS AS A TOXIN IN  
 CC VENOM.  
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-1-THR AND THEN  
 CC ARG-1-ILE BONDS IN PROTHROMBIN TO FORM THROMBIN.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC AND ARE HELD TOGETHER BY A DISULFIDE BOND.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM  
 CC BY SIMILARITY.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR006209; EGF\_Like.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; Vitk\_dep\_GLA.  
 DR Pfam PF00008; EGF; 2.  
 DR Pfam PF00594; gla; 1.  
 DR Pfam PF00089; trypsin; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS00187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Glycoprotein; Hydrolase; Serine protease; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Zymogen; EGF-like domain; Repeat.  
 FT CHAIN 1  
 FT NON\_TER 141  
 FT TER 142  
 FT CHAIN 142  
 FT CHAIN 376  
 FT CHAIN 142  
 FT DOMEIN 50  
 FT DOMEIN 81  
 FT DOMEIN 124  
 FT DOMEIN 376  
 FT MOD\_RES 6  
 FT MOD\_RES 7  
 FT MOD\_RES 14  
 FT MOD\_RES 16  
 FT MOD\_RES 19  
 FT MOD\_RES 20  
 FT MOD\_RES 25  
 FT MOD\_RES 26  
 FT MOD\_RES 29  
 FT MOD\_RES 32  
 FT MOD\_RES 35  
 FT MOD\_RES 63  
 FT ACT\_SITE 183  
 FT ACT\_SITE 229  
 FT ACT\_SITE 326  
 FT ACT\_SITE 376  
 FT DISULFID 17  
 FT DISULFID 50  
 FT DISULFID 61  
 FT DISULFID 72  
 FT DISULFID 81  
 FT DISULFID 89  
 FT DISULFID 96  
 FT DISULFID 109  
 FT DISULFID 111  
 FT DISULFID 124  
 FT DISULFID 132  
 FT DISULFID 168

FT DISULFID 297 311 BY SIMILARITY.  
 FT DISULFID 322 350 BY SIMILARITY.  
 FT CARBOHYD 52 O-LINKED.  
 FT CARBOHYD 186 N-LINKED (GLCNAC...).  
 SQ SEQUENCE 376 AA; 42301 MW; 8484F03AD6B8E17 CRC64;  
 Query Match 42.3%; Score 1114.5; DB 13; Length 376;  
 Best Local Similarity 47.7%; Pred No. 2.7e-100;  
 Matches 209; Conservative 51; Mismatches 107; Indels 71; Gaps 3;  
 QY 41 ANSFLSEEMKKGHLRECEMEETCSYBEAREVFEDSDKTNEFNWKNYKDGQCFETSPQCNQK 100  
 DB 1 SNLFEIIRPGNIERIECEKCSKEAREVFEDNEKTTTFWVYVDGQCSNPCHYRG 60  
 QY 101 CKDGLGEYTCCTCLEGFEKNCCLFTRKLCSLDNGDCQDFCHEQNSVVCSCARGYTLADN 160  
 DB 61 CKDGLGSYTCCTCLPNYEGKNCCKVLFKSCRAFNGCNWHFCKRVQSETQCSAEYSRLVD 120  
 QY 161 GKACIPTGPGCGKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDF 220  
 DB 121 GHSCVAEGDFSGRNKARK----- 141  
 QY 221 NOTQPERGDNNTTRIVGQECQKDCBPQOALLINEENEGFCGGTILSEFYILTAACHLYQ 280  
 DB 142 -----IVNGMDSKLGECBPQOAVLINEKEGEVFCGGTILSPHVLTAACHINQ 187  
 QY 281 AKRFKRVGDRNTEQEEGEAEVHEVYIK-----HNFTKETVDFDIAVLRLKTP 331  
 DB 188 TRSVK-----ETRLLSVDKIYVHTKFVPPNYGCHQNFDRVAYDIDIAIRMKTP 238  
 QY 332 ITRFMNVPACLPEDWAEIETLTKTGIVSGFGRTHKRGROSTRKMKLEVPYVDNRNCK 391  
 DB 239 IQFSENVVPACLPADFAFNEVLKQDSGIVSGFGRIRKEPTNSLTKVITVYVDNRHCTM 298  
 QY 392 LSSFTITQNMFCAGYDKQEDACQDGGSGPHVTRFKDFYFTVGTIVSWGESCARCKGYGI 451  
 DB 299 LSSDFRITQNMFCAGYDTLPQACQDGGSGPHITAYGDTHTFTIVSWGESCARCKGYGV 358  
 QY 452 YTKVTAFLKWDIRSMKTR 469  
 DB 359 YTKVSRFIPWIKMSLK 376  
 RESULT 7  
 O8JHC8 PRELIMINARY; PRT; 474 AA.  
 AC O8JHC8;  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Coagulation factor X.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hanumanthachar R., Day K., Jagadeeswaran P.;  
 RT "Comprehensive analysis of blood coagulation pathways in Teleostei:  
 RT Evolution of coagulation factor genes and identification of zebrafish  
 RT factor VIII";  
 RL Blood Cells Mol. Dis. 0:0-0(2002).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR EMBL; AF519546; AM88343.1; ...  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR001438; EGF\_Like.  
 DR InterPro: IPR006209; EGF\_Like.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR006210; IEGF.



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351 WGRVFKRGRSALVQLYLRVPLVDRLATCLRTKFTIYNNMFCAGFHEGGDRSCQDGGGPH 410
424 VTRFKDQFYVTGIVSGESCARCKYGIYTKVTAFLKWDIRSMK 467
411 VTEVEGTSFLTGIISGECAMKGYIYTKVSRVYNNWIKETK 454

RESULT 9
Q95ND7 PRELIMINARY; PRT; 461 AA.
AC Q95ND7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Satta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL AB062470; BAB58885.1; JOINED.
DR EMBL AB062458; BAB58885.1; JOINED.
DR EMBL AB062460; BAB58885.1; JOINED.
DR EMBL AB062462; BAB58885.1; JOINED.
DR EMBL AB062464; BAB58885.1; JOINED.
DR EMBL AB062466; BAB58885.1; JOINED.
DR EMBL AB062468; BAB58885.1; JOINED.
DR HSP; P00761; IAN1.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR PRINTS; PR00010; EGFbLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLI_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F7F45 CRC64;

Query Match 39.4%; Score 1038.5; DB 6; Length 461;
Best Local Similarity 44.8%; Pred. No. 9.9e-93;
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

QY 9 LLSASLAGLLLCGE-SLFTIRRECANILARVTRANS-FLEEMKKGHLERECMEETCSYEE 66
14 LITCLGLYLLSAECTVFLDENANKILNRPKNYSGKLEEFVQGNLERECMEKCSFEE 73

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Db 20 AVFVRDAHEVLIRKSRANSWFEEELKTNLERECLEKCSYBEAREVFEHTATNEFW 79
QY 82 NKYKDGDCQETSPONQKGC-KDGI GEYTCCTCLEGFEKNCLETRKL---CSLDNGDCD 137
Db 80 KIYDVKDHCASSPCHEHDLCTTQADSYMCLCAPGFSGRHCEQSIGDVPDSCLDHNGCE 139
QY 138 QFCHEEQNVVSCARGVTLADNKGACIPTGYPGCGKOTLERRKSRVAQATSSSGEAPDS 197
Db 140 HFCTEQNGRRNCSCADGYLDNGGKGKSHVFPVCGKVP-----LQAGKAAD- 187
QY 198 ITWKPYDAADLPTENPDLLDFNQTPQERDNNLIRIVGQCKDCECPQWALLINEEN 257
Db 188 -----HQVDL-----RSRIVGSECPKGHCPCWQVLLKYGE- 217
QY 258 EGFCEGCGTILSEFYILTAHCL--YQAKRFKVRVGRDNRTEQEGGEAVEHEVVIKHNFT 315
Db 218 KGFCGGVYKPTWILTAHCLKLVKFLRIVAGEHDLVDEGTEQLIQVDMFTHPAYV 277
QY 316 KETYDFDIATVRLKPTPTFRMNVAPACLPERDWAESTLMTQKTGIVSGFGRTHEKGRST 375
Db 278 SETADSDIALLRLTPTPIVYSYAVPVCLPLREMAERELWAVSKHTVSGWGRKSRSDGPTS 337
QY 376 RLKMLEVYVDRNSKLSSTFIITQNMFCAGYDTKOEDACQDGGSGPHVTRFKDFTYVTG 435
Db 338 LLRLLVPRITQECVQVSNLTLSNMFACGIIEGQDSCCKGDSGGLVTRIDRTAFILG 397
QY 436 IVSWGSCARKGKYGIYTKVTAFLKWDIRSMKT 468
Db 398 IVSWGKGCARPGSYGIYTRVSNYLQWIRQTNT 430

RESULT 14
QYAYE4
ID Q8AYT4 PRELIMINARY; PRT; 503 AA.
AC Q8AYT4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Coagulation factor IX.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthaiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in teleostel:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIII.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
DR EMBL AF515270; AAAT1001.1; -.
SQ SEQUENCE 503 AA; 55905 MW; F127EF35D7A4C1D7 CRC64;

Query Match 35.4%; Score 932; DB 13; Length 503;
Best Local Similarity 40.7%; Pred. No. 3e-82;
Matches 200; Conservative 80; Mismatches 167; Indels 44; Gaps 13;

QY 8 VLLSASLAGLLGLESFIRREQANNILARVTRANSFL-EMKKGHLERECMEETCSYEE 66
Db 12 LLLQNALG-----SVFLDEKADSVLWRRRRANTWLFEEFLPGNVERECIEKCVLEE 64
QY 67 AREVFEDSKTNEFWNKYKDGDCQETSPONQKCKDGLGEYTCCTCLEGFEKNCLEFTR 126
Db 65 AREAPEDEKTEWFAWYVDNGQCKPSPCQNGTCEDQMGYSNCNLCARFCWQNCIEVTA 124
QY 127 KLCSLDNGDCQDFC-----HREQNSVVCARGVTLADNKGACIPTGYPGCGKOTLERRK 181
Db 125 KKCDVDNGGCHBFCHVLESHKTO-----CRVHMDTNSQKMDFTCEPIYKFGCKTSKPAVK 180
QY 182 ----RSVAQATSSSGE-----APDSITWKPDAAD-----LDPTEPNFDLLDFNQ- 222

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Db 181 TFGTASVTNTAQSNNKTIKSTSSIPKPNLT-NPTNSKDIKEKLAPPRAKLPKWAPEY 239
QY 223 -TOPERGDNNL-TRIVYGQCKDCECPWQALLINEENEG-FCGGTILSEFYILTAHCLY 279
Db 240 LTPAPTVSGLSKRIIIGNSALPGEIPWQVALVSRSTQVFCGGSILNPLWITAHCLL 299
QY 280 --CAKRFKVRVGRDNRTEQEGGEAVEHEVVIKHNFTKET--YDFDIATVRLKPTPTFR 335
Db 300 GNHNGSFYIRVGEHDSYKIEGTQENVVDVILKLSHPRYNSKVSFLFNHDIALRLSPILT 359
QY 336 MNVAPACLPERDWAESTLMTQKTGIVSGFGRTHEKGRQSTRKLMLEVPVYVDRNSKLS 395
Db 360 PTVRPLCGPWPFSNTLLQSGTLATVSGWRVRFQGRSAATLQKIELPVLVDRTCKESS 419
QY 396 FIITQNMFCAGYDTKOEDACQDGGSGPHVTRFKDFTYVTGIVSWGSCARKGKYGIYTKV 455
Db 420 DPTHEMFCAHSDSPKDACQDGGSGPHVRYHNTWFLTGIIISWGCECAKKGKYGYTVQV 479
QY 456 TAFELKWDIRSM 466
Db 480 GNYRWRIOHTM 490

RESULT 15
Q61109 PRELIMINARY; PRT; 446 AA.
ID Q61109;
AC Q61109;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Coagulation factor VII.
DE Coagulation factor VII.
DE F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RA MEDLINE=96276538; PubMed=8701412;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996)
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; U44795; AAC52570.1; -.
DR HSSP; P08709; 1FAK.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00003; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE; PS00025; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.

```







CC -1- SUBUNIT: HETEROIDIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- ISSUE SPECIFICITY: Plasma.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC U77477; AAB37326.1; -  
 CC EMBL P08709; IFAK.  
 CC  
 CC MERC S; S01.215;  
 CC Inte Pro; IPR000152; Asx\_hydroxyl.  
 CC Inte Pro; IPR001314; Chymotrypsin.  
 CC Inte Pro; IPR000742; EGF-2.  
 CC Inte Pro; IPR001881; EGF-Ca.  
 CC Inte Pro; IPR001438; EGF-II.  
 CC Inte Pro; IPR006209; EGF-like.  
 CC Inte Pro; IPR002383; GLA\_blood.  
 CC Inte Pro; IPR001254; Ser\_protease\_Try.  
 CC Inte Pro; IPR000294; VitK\_dep\_GLA.  
 CC Pfam PF00008; EGF; 2.  
 CC Pfam PF00594; gla; 1.  
 CC Pfam PF00089; Trypsin; 1.  
 CC PRIN3; PR00722; CHYMOTRYPSIN.  
 CC PRIN3; PR00010; EGF\_blood.  
 CC PRIN3; PR00001; GLABLOOD.  
 CC SMART; SM00179; EGF\_CA; 1.  
 CC SMART; SM00069; GLA; 1.  
 CC SMART; SM00020; Tryp\_Spc; 1.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 1.  
 CC PROSITE; PS01187; EGF\_CA; 1.  
 CC PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 CC PROSITE; PS02040; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 CC Live; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 CC EGF-like domain; Repeat; Signal; Hydroxylation.  
 CC FT SIGNAL 1 21 POTENTIAL.  
 CC FT PROPEP 22 39 POTENTIAL.  
 CC FT CHAT 40 191 FACTOR VII LIGHT CHAIN.  
 CC FT CHAT 192 444 FACTOR VII HEAVY CHAIN.  
 CC FT DOMAN 45 74 GLA-RICH.  
 CC FT DOMAN 85 121 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 CC FT DOMAN 126 167 EGF-LIKE 2.  
 CC FT DOMAN 192 444 SERINE PROTEASE.  
 CC FT SITE 191 192 CLEAVAGE (BY FACTOR XA, FACTOR XIIA,  
 CC ACT SITE 232 232 BY SIMILARITY).  
 CC ACT SITE 281 281 BY SIMILARITY.  
 CC ACT SITE 383 383 BY SIMILARITY.  
 CC BINDING 377 377 SUBSTRATE (BY SIMILARITY).  
 CC BINDING 56 61 BY SIMILARITY.  
 CC DISULFID 89 100 BY SIMILARITY.  
 CC DISULFID 94 109 BY SIMILARITY.  
 CC DISULFID 111 120 BY SIMILARITY.  
 CC DISULFID 130 141 BY SIMILARITY.  
 CC DISULFID 137 151 BY SIMILARITY.  
 CC DISULFID 153 166 BY SIMILARITY.  
 CC DISULFID 174 301 BY SIMILARITY.  
 CC DISULFID 198 203 BY SIMILARITY.  
 CC DISULFID 217 233 BY SIMILARITY.

FT DISULFID 349 368 BY SIMILARITY.  
 FT DISULFID 379 407 BY SIMILARITY.  
 FT MOD\_RES 45 45 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 53 53 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 68 68 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 74 74 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 102 102 HYDROXYLATION (BY SIMILARITY).  
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5427F8 CRC64;  
 Query Match 36.2%; Score 954; DB 1; Length 444;  
 Best Local Similarity 40.2%; Pred. No. 6e-62;  
 Matches 191; Conservative 76; Mismatches 142; Indels 66; Gaps 8;  
 QY 7 LVLSASLAGLLLGESLFIIRREQANNILARYTRANSFLEEMKKGHLERECMEETCSVEE 66  
 Db 13 LLALQASLA-----AVFITQEAHSVLRQRANSFLEELRPGSLERECEKELCSPEE 65  
 QY 67 AREVFEDSKTNEFNKYNKDGDCSTSPCONOGKCKDGLGEYTCCTCLEGFEGKCE--LF 124  
 Db 66 AREVFQSTERTKQFWITYNDGQCASNPQCNGSGCEDQISYICFCLADFEGRNCKNN 125  
 QY 125 TRKLCSLDNGDCDFCHEBQNSV-VCSARGTYTLADNGKACIPTGPGK-OTLERKKR 182  
 Db 126 DQLICMYENGCEQYCSHDHVSQSCRCHEGYTLPLNGVSCPTVDYPCGKVPALKRGA 185  
 QY 183 SYAQATSSSGEAPDSITWKPYPDAALDPTENPFDLLDFNQTPERGDNNLRIVGQBECK 242  
 Db 186 SNPQG-----RIVGKVCVP 199  
 QY 243 DGECPQALLINENEGFCGFTLSEFYLTAAHC---LYOAKRFKVRVGRDNTQEREGG 299  
 Db 200 KGECPQQAALNGSTL-LCGGSLDTHWVVSNAHCFDKLSLRNLTIVLGEHDLSEHGD 258  
 QY 300 EAVHEVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTOKTG 359  
 Db 259 EQVRHVAQLIMPDKYVPGKTDHDIALLRLQPAALTNVPLCPERNFSESTLATIRFS 318  
 QY 360 IVSGFRGTHGROSTRKMLKLEVPYVDNRNSCKLSS-----SFIITQNFACAGYDTKQEDA 414  
 Db 319 RVSGWQQLLYRGALARELMAIDVPRMTQDCVEOSEHKPGSPVETGNMFCAGYLDGSKDA 378  
 QY 415 CQDSDGGPHVTRFKDITYEVTGIVSWGESCARKGYGIYTKVTAFLKWDIRSMKTR 469  
 Db 379 CKGDSGGPHATSYHGTWLTGTVSWGEGCAAVGHVGVYTRVSRYTEWLSRLMRSK 433  
 RESULT 11  
 FA7\_HUMAN STANDARD; PRT; 466 AA.  
 ID FA7\_HUMAN  
 AC P08709; Q14339;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
 DE conversion accelerator) (Bptacog alfa).  
 GN F7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid-9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86205965; PubMed=3486420;

DR	PIR: AL4757; KFB0.	Query Match	36.6%; Score 963; DB 1; Length 416;
DR	HSSP: P00740; ICFH.	Best Local Similarity	43.3%; Prod. No. 1.2e-62;
DR	MERCOS; S01.214; .	Matches	188; Conservative 70; Mismatches 140; Indels 36; Gaps 8;
DR	GLYCOSuiteDB; P00741; .		
DR	Inte-Pro; IPR000152; Asx_hydroxyl.	QY	45 LEMKKGHLEECMEETCSYEAREVFEEDSDKTNEFWNKKYKDGQDQCECSPCQNOGCKDKG 104
DR	Inte-Pro; IPR0001314; Chymotrypsin.	Db	6 LEEFVRGNLERCKEKEKCSFEAREVFENTKTEFWKQYVDGQCESNCLNGGCKDD 65
DR	Inte-Pro; IPR000742; EGF_2.	QY	105 LGEYTCCTCLEGPEGKNCLEFTRKCLSLDNGDCDOFC-HEEONSVVVSCARGYTLADNGKA 163
DR	Inte-Pro; IPR001881; EGF-Ca.	Db	66 INSEWCQAGFEGTNCEL--DATSIKNGRCQFKRDTDNKVKVSCSDTGYLAEDQKS 123
DR	Inte-Pro; IPR001438; EGF-II.	QY	164 CIPTPGPGCQKQLERRKRSVAQA-----TSSSGEAPDSITWPKYDAADLPTENPFDL 217
DR	Inte-Pro; IPR006209; EGF-like.	Db	124 CEPVFPFCGRVSVSHSKLTRAETIFSNNTVNSSEAEIWD----- 167
DR	Inte-Pro; IPR002383; GLA_blood.	QY	218 LDFNQTPERGDNLNIRIVGGQCKGECPCWQALLINEEGPCGFTILSEFVILTAHC 277
DR	Inte-Pro; IPR001254; Ser. protease_Try.	Db	168 ---NVTQSNQSFDEFKRVVGGDEAERGQFPQVLL-HGEIAFCGGSIVNEKVVVTAHC 223
DR	Inte-Pro; IPR000294; VitK_dep_GLA.	QY	278 LYQAKRFKRVGRDNRTEOEGGEAVHEVEVVIKHNFTK--ETYDFDIAVLRKLTPTTR 335
DR	Pfam PF00008; EGF; 2.	Db	224 IKGVKITVVAGEHTEKPEPTQKRVIRAIYPHSYNASINKYSHDIALLEDEPLELN 283
DR	Pfam PF00594; gla; 1.	QY	336 MNVAPACLPERDWAESTLMTQK--TGIVSGFGRTHKRGOSTRLKMLEVPYVDNRNCKLS 393
DR	Pfam PF00089; trypsin; 1.	Db	284 SYVTPICIADRDY---TNIFSKFGYGVYSGWGVNFRGRSASITQVLKPLVDVDRATCLRS 340
DR	PRIN_S; PR00722; CHYMOTRYPSIN.	QY	394 SSTIITQMFACGYDKQEDACOGDGGPHVTRFKDTFYVTGIVSGWESCARCKGYIYT 453
DR	PRIN_S; PR00010; EGF_BLOOD.	Db	341 TKFSIYSHMFCAGYHGGKSCODSGGPHVTEVEGTSFLTGIIISWGECAMKGYIYT 400
DR	PRIN_S; PR00001; GLABLOOD.	QY	454 KVTAFKLWIDRSMK 467
DR	SMAR; SM00179; EGF_CA; 1.	Db	401 KVSRYVNWIKETK 414
DR	SMAR; SM00069; GLA; 1.		
DR	SMAR; SM00020; TRYP_SPC; 1.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.		
DR	PROSITE; PS00022; EGF_1; 1.		
DR	PROSITE; PS01186; EGF_2; 2.		
DR	PROSITE; PS01187; EGF_CA; 1.		
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.		
DR	PROSITE; PS05240; TRYPsin_DOM; 1.		
DR	PROSITE; PS00134; TRYPsin_HIS; 1.		
DR	PROSITE; PS00135; TRYPsin_SER; 1.		
KW	Blood coagulation; Plasma; Serine protease; Calcium-binding;		
KW	Hydrolase; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid;		
KW	Hemophilia; Hydroxylation; Zymogen; EGF-like domain.		
FT	CHAI 1 146	RESULT 10	
FT	PROPEP 147 181	FA7_RABIT	
FT	CHAI 182 416	ID FA7_RABIT STANDARD; PRT; 444 AA.	
FT	DOMAN 47 83	AC P98139; P79224;	
FT	DOMAN 84 125	DT 01-FEB-1996 (Rel. 33, Created)	
FT	DOMAN 182 416	DT 15-JUL-1998 (Rel. 36, Last sequence update)	
FT	SITE 146 181	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
FT	SITE 181 182	DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin	
FT	MOD_RES 7 7	DE conversion accelerator).	
FT	MOD_RES 8 8	GN F7.	
FT	MOD_RES 15 15	OS Oryctolagus cuniculus (Rabbit).	
FT	MOD_RES 17 17	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
FT	MOD_RES 20 20	OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.	
FT	MOD_RES 21 21	OC NCB1_TaxID=9986;	
FT	MOD_RES 26 26	RP SEQUENCE FROM N.A.	
FT	MOD_RES 27 27	RC TISSUE=Liver;	
FT	MOD_RES 30 30	RX MEDLINE=93190306; PubMed=8383365;	
FT	MOD_RES 33 33	RA Brothers A.B.; Clarke B.J.; Sheffield W.P.; Blajchman M.A.;	
FT	MOD_RES 36 36	RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation	
FT	MOD_RES 40 40	RL factor VII.";	
FT	MOD_RES 44 64	RL Thromb. Res. Suppl. 69:231-238(1993).	
FT	MOD_RES 51 62	RP BY SIMILARITY.	
FT	MOD_RES 56 71	RC TISSUE=Liver;	
FT	MOD_RES 73 82	RC REVISION TO 395.	
FT	MOD_RES 88 99	RA Ruiz S.R.; Blajchman M.A.; Clarke B.J.;	
FT	MOD_RES 95 109	RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.	
FT	MOD_RES 111 124	CC -!- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS	
FT	CARBOHYD 53 53	CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XI, FACTOR IXA, OR	
FT	CARBOHYD 158 158	CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR	
FT	CARBOHYD 168 168	CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA	
FT	CARBOHYD 173 173	CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO	
FT	CARBOHYD 261 261	CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY	
FT	ACT_SITE 222 222	CC SIMILARITY).	
FT	ACT_SITE 270 270	CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -lle bond in factor X to	
FT	ACT_SITE 366 366	CC form factor Xa.	
FT	ACT_SITE 64 64		
FT	VARIANT 416 AA; 46785 MW; 34A7DFE916330662 CRC64;		
FT	SEQUENCE		

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FT MOD_RES 69 69 (BY SIMILARITY).
FT FT GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 72 72 (BY SIMILARITY).
FT FT GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 75 75 (BY SIMILARITY).
FT FT GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 79 79 (BY SIMILARITY).
FT FT GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 103 103 (BY SIMILARITY).
FT FT HYDROXYLATION (BY SIMILARITY).
FT DISULFID 57 62 (BY SIMILARITY).
FT DISULFID 90 101 (BY SIMILARITY).
FT DISULFID 95 110 (BY SIMILARITY).
FT DISULFID 112 121 (BY SIMILARITY).
FT DISULFID 127 138 (BY SIMILARITY).
FT DISULFID 134 148 (BY SIMILARITY).
FT DISULFID 150 163 (BY SIMILARITY).
FT CARBHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT ACT_SITE 258 258 CHARGE RELAY SYSTEM.
FT ACT_SITE 306 306 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT VARIANT 418 418 G -> E (IN HEMOPHILIA B).
SQ SEQUENCE 452 AA; 50627 MW; 1F6537C46A6960ED CRC64;

Query Match 39.2%; Score 1032.5; DB 1; Length 452;
Best Local Similarity 44.6%; Pred. No. 1.3e-67;
Matches 207; Conservative 81; Mismatches 151; Indels 25; Gaps 10;

QY 9 LLSASLACGLLLGE-SUFIREQANNILARVTRANS-FLEMKKGHLERSCMETCSYEE 66
Db 7 LVTVCLLGYLLSACAVFLDRENATKILSRPKRYNSGKLEFVRGNLERECIERKCSFEE 66
QY 67 AREVFESDKTNEFWNKYKGDQCTSPCONOGKCKDGLGCTCTCLEGFEGRKNCLEFTR 126
Db 67 AREVFENTEKTTEFWNKYVDGQCESNPLNDGVCDDINSYECWCRAGFEGRKNCLELV- 125
QY 127 KCLSDNGDCQDFCH-BEQNSVVCARGTYLADNGKACIPTGYPYCGKQTLERRKRSVA 185
Db 126 -TCNIKNRGKQFCGLDGNKVCSCCTGYQLAEDQRCEPAPVFPFCGRVSVPHISMT 184
QY 186 QATSSSGEAPDSITWKPYDAADLPOTENPFLLDFNOTOPERGDNNTLRIVGGECKDGE 245
Db 185 RAETL-----FSNMDYENSTEVEKILD-NVTQPL---NDFTRVYVGKDAKPGQ 228
QY 246 CPWQALLINEEGFCGCTILSEFYILTAACHLYQAARFKRVGRVDRNTEOEGGEAVHEV 305
Db 229 FPMQVLL-NGKVDAFCGSIINEKVVVTAARHICIEPDVKIIVAGEHTEKREHTQKRV 287
QY 306 EVVYKHNRFF--TKETYDFDIARLKTPTIFRMNVAPACLPERDWAESTLMTQKTGVSG 363
Db 288 IRTILHHSYNATINKYNHDIALLLEBPLTNSVVTPTCIADREYS-NIELKFGSGYVSG 346
QY 364 FGRTHKGROSTRLEKVPVVDNRNSCKLSSEFIITONMFCAGVDTKQEDACOGDSGGPH 423
Db 347 WGRVFNKGRSASILQYKLVPLVDRLCTLRSTKFTIYNNMFCAGFHEGKDCQGDGSGPH 406
QY 424 VTRFKDTYFVTVGIVSWGECARKGKGYITKVTAFKWDIRSMK 467
Db 407 VTEVEGISFLTGIIISWGECAMKGYITKVSRYVNWIREKT 450

RESULT 9
FA9_BOVIN
ID FA9_BOVIN STANDARD; PRT; 416 AA.
AC P0071;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor IX (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Bos taurus (Bovine).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos; NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80056619; PubMed=291916;
RA Katayama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H.,
RA Davie E.W., Titani K.;
RT "Comparison of amino acid sequence of bovine coagulation Factor IX
RT (Christmas Factor) with that of other vitamin K-dependent plasma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4990-4994(1979).
RN [2]
RP REVISION TO 64.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [3]
RP SEQUENCE OF 51-111 FROM N.A.
RX MEDLINE=82272386; PubMed=6287289;
RA Choo K.H., Gould K.G., Rees D.J.G., Brownlee G.G.;
RT "Molecular cloning of the gene for human anti-haemophilic factor IX.";
RL Nature 299:178-180(1982).
RN [4]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
RT blood coagulation factors VII and IX.";
RL J. Biochem. 104:867-868(1988).
RN [5]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-53.
RX MEDLINE=90130422; PubMed=2105311;
RA Hase S., Nishimura H., Kawabata S., Iwanaga S., Ikenaka T.;
RT "The structure of (xylose)2glucose-O-serine 53 found in the first
RT epidermal growth factor-like domain of bovine blood clotting factor
RT IX.";
RL J. Biol. Chem. 265:1858-1861(1990).
CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA(2+)
CC IONS, PHOSPHOLIPIDS, AND FACTOR VIII.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa, WHICH EXCISES THE
CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID
CC (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE,
CC BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00007; AAA30520.1; -

```



	PROSITE; PS01186; EGF_2; 2.	1	BY SIMILARITY.
DR	PROSITE; PS01187; EGF_CA; 1.	<1	
DR	PROSITE; PS00011; GLU-CARBOXYLATION; 1.	17	
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.	35	FACTOR IXA (ACTIVE FORM) LIGHT CHAIN.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	180	ACTIVATION PEPTIDE.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	225	FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
KW	Blood coagulation; Plasma; Serine protease; Calcium-binding;	81	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
KW	Hydrolase; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid;	118	EGF-LIKE 2.
KW	Hemophillia; Hydroxylation; Zymogen; Signal; EGF-like domain;	225	SERINE PROTEASE.
KW	Repeat.	180	CLEAVAGE (BY FACTOR XIA) (BY SIMILARITY).
FT	NON_TER	224	CLEAVAGE (BY FACTOR XIA) (BY SIMILARITY).
FT	SIGNAL	41	GAMMA-CARBOXYGLUTAMIC ACID
FT	PROPEP	42	(BY SIMILARITY).
FT	CHAIN	49	GAMMA-CARBOXYGLUTAMIC ACID
FT	PROPEP	51	(BY SIMILARITY).
FT	CHAIN	54	GAMMA-CARBOXYGLUTAMIC ACID
FT	DOMAIN	55	(BY SIMILARITY).
FT	DOMAIN	60	GAMMA-CARBOXYGLUTAMIC ACID
FT	DOMAIN	61	(BY SIMILARITY).
FT	SITE	64	GAMMA-CARBOXYGLUTAMIC ACID
FT	SITE	67	(BY SIMILARITY).
FT	MOD_RES	70	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES	74	(BY SIMILARITY).
FT	MOD_RES	98	GAMMA-CARBOXYGLUTAMIC ACID
FT	ACT_SITE	265	(BY SIMILARITY).
FT	ACT_SITE	313	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	409	CHARGE RELAY SYSTEM.
FT	DISULFID	52	CHARGE RELAY SYSTEM.
FT	DISULFID	57	BY SIMILARITY.
FT	DISULFID	85	BY SIMILARITY.
FT	DISULFID	90	BY SIMILARITY.
FT	DISULFID	107	BY SIMILARITY.
FT	DISULFID	122	BY SIMILARITY.
FT	DISULFID	129	BY SIMILARITY.
FT	DISULFID	145	BY SIMILARITY.
FT	CARBOHYD	192	N-LINKED (GLCNAC. . ) (POTENTIAL).
FT	CARBOHYD	211	N-LINKED (GLCNAC. . ) (POTENTIAL).
FT	CARBOHYD	304	N-LINKED (GLCNAC. . ) (POTENTIAL).
FT	CONFLICT	363	H -> Q (IN REF. 2).
FT	CONFLICT	388	T -> I (IN REF. 2).
FT	SEQUENCE	459 AA; 51635 MW; EP439C840D6CBC1A CRC64;	
SQ	Best Match	39, 58; Score 1039.5; DB 1; Length 459;	
	Query Local Similarity	44.4%; Pred. No. 4e-68;	
	Matches 211; Conservative	78; Mismatches 151; Indels 35; Gaps 11	
OY	9 LLASLAGLLLGE-SLFIRREQANNTIARVTRANS-FLEMKKGHLECHEMETSCEE 66		
Ddb	2 LITIFLLGYLLSTECVFLDENATKILTRPKRYNSKLEEFGVGNLRCEIECRSFEE 61		
OY	67 AREVFESDKTNFWNKYGDDGQCFSPONQCKGDGLGEYTCCTCLEGFEGKNCELFTFR 126		

RP CALCIUM-BINDING DATA.  
 RX MEDLINE=84185715; PubMed=6425296;  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RT "Derivatives of blood coagulation factor IX contain a high affinity  
 RT Ca2+ binding site that lacks gamma-carboxyglutamic acid.";  
 RL J. Biol. Chem. 259:5698-5704(1984).  
 RN [131]  
 RN ERRATA.  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RL J. Biol. Chem. 260:2583-2583(1985).  
 RN [141]  
 RN SIGNAL SEQUENCE CLEAVAGE SITE.  
 RP MEDLINE=86189947; PubMed=3009023;  
 RX Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;  
 RA "Defective propeptide processing of blood clotting factor IX caused  
 RT by mutation of arginine to glutamine at position -4.";  
 RL Cell 45:343-348(1986).  
 RN [151]  
 RN STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=90062160; PubMed=2511201;  
 RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RN [161]  
 RN STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [171]  
 RN STRUCTURE OF CARBOHYDRATE ON SER-107.  
 RX MEDLINE=92388094; PubMed=1517205;  
 RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;  
 RT "Human factor IX has a tetrasaccharide O-glycosidically linked to  
 RT serine 61 through the fucose residue.";  
 RL J. Biol. Chem. 267:17520-17525(1992).  
 RN [181]  
 RN PHOSPHORYLATION OF SER-114.  
 RA Harris R.J., Papac D.I., Truong L., Smith K.J.;  
 RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";  
 RL (In) Abstracts of Xth international conference on methods in protein  
 RL structure analysis, pp.50-50, Annecy (1996).  
 RN [191]  
 RN TRANSLATIONAL MODIFICATIONS.  
 RP POST MEDLINE=20575397; PubMed=11133752;  
 RX Arru V.R., Hagstrom J.N., Deitch J., Heiman-Patterson T.,  
 RA Camille R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,  
 RA Larsen P.J., High K.A.;  
 RT "Posttranslational modifications of recombinant myotube-synthesized  
 RT human factor IX.";  
 RL Blood 97:130-138(2001).  
 RN [201]  
 RN STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=95229607; PubMed=7713897;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane  
 RT binding region of factor IX by two-dimensional NMR spectroscopy.";  
 RL J. Biol. Chem. 270:7980-7987(1995).  
 RN [211]  
 RN STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=96032604; PubMed=7547952;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich  
 RT domain of factor IX.";  
 RL Biochemistry 34:12126-12137(1995).  
 RN [221]  
 RN STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=96279169; PubMed=8663165;

RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,  
 RA Furie B.;  
 RT "Identification of the phospholipid binding site in the vitamin K-  
 RT dependent blood coagulation protein factor IX.";  
 RL J. Biol. Chem. 271:16227-16236(1996).  
 RN [231]  
 RN STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=97199336; PubMed=9047312;  
 RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,  
 RA Smith H., Hiskey R.G., Pedersen L.G.;  
 RT "Refinement of the NMR solution structure of the  
 RT gamma-carboxyglutamic acid domain of coagulation factor IX using  
 RT molecular dynamics simulation with initial Ca2+ positions determined  
 RT by a genetic algorithm.";  
 RL Biochemistry 36:2132-2138(1997).  
 RN [241]  
 RN STRUCTURE BY NMR OF 91-133.  
 RX MEDLINE=91308127; PubMed=1854745;  
 RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;  
 RT "Sequence-specific 1H NMR assignments, secondary structure, and  
 RT location of the calcium binding site in the first epidermal growth  
 RT factor like domain of blood coagulation factor IX.";  
 RL Biochemistry 30:7402-7409(1991).  
 RN [251]  
 RN STRUCTURE BY NMR OF 92-130.  
 RX MEDLINE=93284090; PubMed=1304885;  
 RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,  
 RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;  
 RT "The three-dimensional structure of the first EGF-like module of  
 RT human factor IX: comparison with EGF and TGF-alpha.";  
 RL Protein Sci. 1:81-90(1992).  
 RN [261]  
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.  
 RX MEDLINE=95330802; PubMed=7606779;  
 RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;  
 RA Query Match 39.5%; Score 1041.5; DB 1; Length 461;  
 RA Best Local Similarity 44.8%; Pred. No. 2.9e-68; Indels 23; Gaps 10;  
 RA Matches 208; Conservative 76; Mismatches 157;  
 QY 9 LLSASLAGLLLGE-SLFIRREQANNILARVTRANS-FLEEMKKGHLERECMEETSCEE 66  
 DB 14 LITICLLGYSAAECTVFLDHENANKILNRPKRYNSGKLEEFVQGNLERECMEKCSFEE 73  
 QY 67 AREVFESDKTNEFNWYKGDQCEPSCNOGCKGGLGYCTCLGEGKNCLEFTR 126  
 DB 74 AREVFENTERTEFWKQYVDGQCESNPCLNGSGCKDDINSYECWCFEGEGKNCLEFTR 132  
 QY 127 KLCSLDNGDCDFC-HEEQNSVVCSCARGVTLADNGKACIPTGPGCKOTLERRKRSVA 185  
 DB 133 -TCNIKNGRCQFCNKADNKNVCSCTEGYLAENQKSCPEAVFPFGGRVSVSQ---TS 187  
 QY 186 QATSSSGEAPDSITWKPYDAADLPTEPNPDLDFNOTQPERGDNNTTRIVGGCECKDGE 245  
 DB 188 KLTRAFAVFPD-----VDYVNSTAEATILD---NITQSTQSFNDFTRVVGSDAKPGQ 237  
 QY 246 CPWQALLNEENEGCGTILSEFYILTAACHLYOAKRFKVRVGDRTNTEOEGGEAVHEV 305  
 DB 238 FPWQVVL-NGKVDACGGSIVNKKWIVTAACHVETGKIVTVAGEHNEETEHTQKRVN 296  
 QY 306 EWLTKHNRFTK--ETDFDIAVLRKLTPTIFRMNVAPACLPERDWAESTLMTQKTYGVSG 363  
 DB 297 IRIIPHHYNAANKYNDHIALLEDEPLVNSVYTPICIADEKVT-NIFLFGSGYVSG 355  
 QY 364 FGRTHEKGRQSTRKLMLEVPVYDRNSKLSSTFIITQNMFCAGYDTKOEDACQDGGPH 423  
 DB 356 WGRVPHKRSALVQLVPLVDRATCLRSKFTIYNMFCAGHEGDRSCQDGGPH 415  
 QY 424 VTRPKDTVFVGVISWGESCARKGYIYTKVTAFLKWDKSMK 467  
 DB 416 VTEVEGTSFLTGLTISWGECAMKGYIYTKVSRVNVWIKETK 459

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FT DISUFID 50 61 BY SIMILARITY.
FT DISUFID 55 70 BY SIMILARITY.
FT DISUFID 72 81 BY SIMILARITY.
FT DISUFID 89 100 BY SIMILARITY.
FT DISUFID 96 109 BY SIMILARITY.
FT DISUFID 111 124 BY SIMILARITY.
FT DISUFID 132 249 INTERCHAIN (BY SIMILARITY).
FT DISUFID 148 153 BY SIMILARITY.
FT DISUFID 168 184 BY SIMILARITY.
FT DISUFID 297 311 BY SIMILARITY.
FT DISUFID 322 350 BY SIMILARITY.
FT CARBYHD 52 52 O-LINKED. (GLCNAC. .).
FT CARBYHD 186 186 N-LINKED. (GLCNAC. .).
SQ SEQUENCE 376 AA; 42455 MW; F5A5C7FE9BA561C1 CRC64;

Query Match
Best Local Similarity 43.1%; Score 1135.5; DB 1; Length 376;
Matches 209; Conservative .55; Mismatches 103; Indels 71; Gaps 3;

QY 41 ANSFLEEMKGLERECHEETCSYEAREVEFEDSDKTNEFWNKYKGDQCETSPCQNGK 100
Db 1 SNSFEETRPNGIERECTEERCSKEAREVEFEDNEKTETFWNVYVDGQCSNPNCHYRGT 60

QY 101 CKDGLGTCCTLEGFECKNCELFTFKLCSLDNGDCDOFCHEEQNSVVCSCARGYTLADN 160
Db 61 CKDGLGTCCTCLPNYEGKCEKVLQSCRYDNGNCWHFCRKRVSQTCSCAESYRLGVD 120

QY 161 GKACIPTGPGKQOTLERRKRSVAQATSSSGEAPDSITWKPYPDAADLDPTENPFDLLDF 220
Db 121 GHSCVAEGDFSGRNIKARNK----- 141

QY 221 NOTQPERGDNLTRVGOEGCKGDCGCPWQALLINEEGFCGGTILSEFILTAAHCLYQ 280
Db 142 -----IVNGMCKLCEGCPWQAVLINEGCVFGGTILSPIHLVTAACHINQ 187

QY 281 AKRFKVRVGRDRTQEGEGEAVHEVEVVK-----HNRFTKTYDEDIAVLRLKTP 331
Db 188 TKSVK-----ETRELLSVDKIYVHTKFPVNPYVYVQNFDRVAYDIALIRMKTP 238

QY 332 ITRFNVYAPACLPEDNAESTLTKQTVISGFGFQRTHEKGRQSTRKMLLEVYPVDRNSCK 391
Db 239 IOFSENVVAPCLPADFANEVLMKQDSGIVSGFGFQRTHEKGRQSTRKMLLEVYPVDRNSCK 298

QY 392 LSSSFIITQNFACGYDTQBDACQDGGPHVTRFKDTYFTVIGVSWGESCKARKKYGI 451
Db 299 LSSDFRITQNFACGYDTLPQDACQDGGPHVTRFKDTYFTVIGVSWGESCKARKKYGI 358

QY 452 YTKVTAFLKWDTRSMKTR 469
Db 359 YTKVSKFIPWIKIMSLK 376

RESULT 6
FA9_HUMAN
ID FAS_HUMAN STANDARD; PRT; 461 AA.
AC P00740;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86000558; PubMed=2994716;
RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
RT "Nucleotide sequence of the gene for human factor IX (antithromphillc factor B).";
RL Biochemistry 24:3736-3750(1985).
RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE=85190593; PubMed=3857619;
RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
RA Graham J.B., Stafford D.W.;
RT "Evidence for a prevalent dimorphism in the activation peptide of
RL human coagulation factor IX.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236100; PubMed=6329734;
RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,
RA Huddleston J.A., Brownlee G.G.;
RT "The gene structure of human anti-haemophilic factor IX.";
RL EMBO J. 3:1053-1060(1984).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=83220788; PubMed=6687940;
RA Jaye M., de la Salle H., Schamber F., Balland A., Kohli V.,
RA Findeli A., Tolstoshev P., Lecocq J.P.;
RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a
RT unique 52-base synthetic oligonucleotide probe deduced from the amino
RT acid sequence of bovine factor IX.";
RL Nucleic Acids Res. 11:2325-2335(1983).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS THR-194 AND PRO-461.
RA Rieder M.J., Amel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 36-326 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=84300526; PubMed=6089357;
RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;
RT "Isolation and characterization of human factor IX cDNA:
RT identification of Tag I polymorphism and regional assignment.";
RL Somat. Cell Mol. Genet. 10:465-473(1984).
RN [7]
RP SEQUENCE OF 290-359 FROM N.A.
RX MEDLINE=88127096; PubMed=3340835;
RA Stoflet E.S., Koeberl D.D., Sarkar G., Sommer S.S.;
RT "Genomic amplification with transcript sequencing.";
RL Science 239:491-494(1988).
RN [8]
RP SEQUENCE OF 444-461 FROM N.A.
RX MEDLINE=94054330; PubMed=8236150;
RA de la Salle C., Charmanier J.L., Baas M.J., Schwartz A.,
RA Wiesel M.L., Grunbaum L., Cazenave J.-P.;
RT "A deletion located in the 3' non translated part of the factor IX
RT gene responsible for mild haemophilia B.";
RL Thromb. Haemost. 70:370-371(1993).
RN [9]
RP SEQUENCE OF 47-461 (VARIANT NAGOYA).
RX MEDLINE=90078229; PubMed=2592373;
RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
RA Ogata K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
RT trypophan and its activation by alpha-chymotrypsin and rat magt cell
RT chymase.";
RL J. Biol. Chem. 264:21257-21265(1989).
RN [10]
RP HYDROXYLATION OF ASP-110.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [11]
RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=78194509; PubMed=659613;
RA di Scipio R.G., Kurachi K., Davie E.W.;
RT "Activation of human factor IX (Christmas factor).";
RL J. Clin. Invest. 61:1528-1538(1978).
RN [12]

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FT	ACT_SITE	425	425	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	90	101	BY SIMILARITY.
FT	DISULFID	95	110	BY SIMILARITY.
FT	DISULFID	112	121	BY SIMILARITY.
FT	DISULFID	129	140	BY SIMILARITY.
FT	DISULFID	136	152	BY SIMILARITY.
FT	DISULFID	154	167	BY SIMILARITY.
FT	DISULFID	175	348	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	247	252	BY SIMILARITY.
FT	DISULFID	267	283	BY SIMILARITY.
FT	DISULFID	396	410	BY SIMILARITY.
FT	DISULFID	421	449	BY SIMILARITY.
FT	CARBHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	207	207	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	228	228	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	285	285	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	475 AA; 53142 MW; 570BF84956C5C74D CRC64;		
Query Match 54.1%; Score 1425; DB 1; Length 475;				
Best Local Similarity 55.3%; Pred. No. 5.2e-96;				
Matches 267; Conservative 71; Mismatches 123; Indels 22; Gaps 4;				
QY	1	MGRPLHLVLSASLAGLLLGESLFIIRQOANNILARVTRANSFLEMKGHLERCMEE	60	
DB	1	MAGRLLLLLLCAALPDELRAEGGVFIKKSADKFLERTKRANSFLEMKOGNIERCNEE	60	
QY	61	TCSVEAREVPEFSDKTFNEWNYKDGDCQETSPCQNGKCKDGLGEYTCCTLEGPEGKN	120	
DB	61	RCSEAREAFEDNEKTEEFENWYVGDQCSNPNHYGGCKDGLGYTCCLDGYGQKN	120	
QY	121	CELETRKCLSDNGDCDQFC---HEEQNSVVCSCARGYTLADNGKACIPGYPGCKQTL	177	
DB	121	CEFVPIPKYCKINNGDCEQFCISIKSVQKDVVCSCTSGYLAEDGKQCVSKVYPCGRVLM	180	
QY	178	ERRKRSVAQTSSEAPDSITWPKYDAALDPT-----ENPDLDFNQTQPERGNNL	232	
DB	181	KRIKRSVILTPNSNTATSD-----QDVPSTNGSILEEFTTTTSTPTPPRNGSSI	232	
QY	233	-----TRVGGQCKGCECPQWALLNEEGFCGTTILSERVILTAACHLQAKRFV	286	
DB	233	TDPNVDTTRVGGDCRGCCEPQWAVLNEKEEFCGTTILNEDFILTAAHCINGSKELV	292	
QY	287	RVGDRNTBQEGGEAVHEVEVVIKHNFTKETDYDFDIAVLRLKTPITFRMNVAPACLP	346	
DB	293	VVGEVDREKEHSETHTAETAEKIFVHSYIAETDNDIALIKKEPIQSEVVPACLPQA	352	
QY	347	DWAESTLMTQITGVSGFGRTHKRGROSTRKLKMLEVPYVDRNSCKLSSFLITONMFCAG	406	
DB	353	DFANEVLNMQSGMVSGFGEAGRLSKRLKLVLEVPYVDRSTCKSTNFATENMFCAG	412	
QY	407	YDTKOEDACQDGGSPHVTFRKDYFVTGIVSWGSCARKGKYGIYTKVTAFLKWDISM	466	
DB	413	YETQKDACQDGGSPHVTFRKDYFVTGIVSWGSCARKGKYGIYTKLSRFLRWRTVM	472	
QY	467	KTR 469		
DB	473	RQK 475		
RESULT 5				
FA10	TROCA	STANDARD;	PRT;	376 AA.
AC	P81428;			
DT	30-MAY-2000	(Rel. 39, Created)		
DT	30-MAY-2000	(Rel. 39, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Coagulation factor X (EC 3.4.21.6) (trocarin prothrombin activator).			
OS	Tropidichis carinatus (Australian rough-scaled snake).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidoptera; Squamata; Scleroglossa; Serpentes; Colubroides;			
OC	Elapidae; Notechidae; Tropidichis.			
OX	NCBI:TaxID=100989;			
RN	[1]			

SEQUENCE, AND CHARACTERIZATION.

TISSUE-Venom;

MEDLINE-99326314; PubMed=10397729;

Joseph J.S., Chung M.C.M., Jayaseelan K., Kini R.M.;

\*Amino acid sequence of trocarin, a prothrombin activator from

Tropidichis carinatus venom: its structural similarity to coagulation

factor Xa.\*;

Blood 94:621-631(1995).

- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that

converts prothrombin to thrombin in the presence of factor Va,

calcium and phospholipid during blood clotting. Acts as a toxin

in venom.

- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then

Arg-|-Ile bonds in prothrombin to form thrombin.

- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.

- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME

GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

CALCIUM.

- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE

INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

- SIMILARITY: Contains 2 EGF-like domains.

HSSP; P00742; IHCG.

MEROPS; S01.216; .

InterPro; IPR000152; Asx\_hydroxyl.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR000742; EGF\_2.

InterPro; IPR001881; EGF\_Ca.

InterPro; IPR001438; EGF\_II.

InterPro; IPR006209; EGF\_like.

InterPro; IPR002383; GLA\_like.

InterPro; IPR001254; Ser\_protease\_Try.

InterPro; IPR000294; VitK\_dep\_GLA.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00010; EGFBLD.

PRINTS; PR00001; GLABLOD.

SMART; SM00179; EGF\_CA; 1.

SMART; SM00069; GLA; 1.

SMART; SM00020; Tryp\_SPC; 1.

PROSITE; PS00010; ASX\_HYDROXYL; 1.

PROSITE; PS00022; EGF\_1; 1.

PROSITE; PS01187; EGF\_CA; 1.

PROSITE; PS00011; GLU\_CARBOXYLATION; 1.

PROSITE; PS02040; TRYPSIN\_DOM; 1.

PROSITE; PS00134; TRYPSIN\_HIS; 1.

PROSITE; PS00135; TRYPSIN\_SER; 1.

Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;

gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;

Zymogen; EGF-like domain; Repeat.

CHAIN	1	141	FACTOR X LIGHT CHAIN.
NON_CONS	141	142	
CHAIN	142	376	FACTOR X HEAVY CHAIN.
CHAIN	142	376	ACTIVATED FACTOR XA, HEAVY CHAIN.
DOMAIN	50	81	EGF-LIKE 1, CALCIUM-BINDING.
DOMAIN	89	124	EGF-LIKE 2.
DOMAIN	142	376	SERINE PROTEASE.
MOD_RES	6	6	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	7	7	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	14	14	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	16	16	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	19	19	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	20	20	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	25	25	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	26	26	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	29	29	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	32	32	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	35	35	GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES	63	63	HYDROXYLATION (BY SIMILARITY).
ACT_SITE	183		CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	229		CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	326		CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	326		BY SIMILARITY.
DISULFID	17	22	





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 [10] STRUCTURE BY NMR OF 85-126.  
 MEDLINE=91084483; PubMed=2261466;  
 Sella der M., Persson E., Stenflo J., Drakenberg T.,  
 "1H NMR assignment and secondary structure of the Ca2(+)-free form of  
 the amino-terminal epidermal growth factor like domain in coagulation  
 factor X";  
 Biochemistry 29:8111-8118 (1990).  
 [11] Biochemistry 29:8111-8118 (1990).  
 STRUCTURE BY NMR OF 85-126.  
 MEDLINE=92329412; PubMed=1627540;  
 Ullner M., Sella der M., Persson E., Stenflo J., Drakenberg T.,  
 Teleman O.;  
 "Three-dimensional structure of the apo form of the N-terminal  
 EGF-like module of blood coagulation factor X as determined by NMR  
 spectroscopy and simulated folding";  
 Biochemistry 31:5974-5983 (1992).  
 [12] Biochemistry 31:5974-5983 (1992).  
 STRUCTURE BY NMR OF 85-126.  
 MEDLINE=92406922; PubMed=1527084;  
 Sella der M., Ullner M., Persson E., Teleman O.,  
 Stenflo J., Drakenberg T.;  
 "How an epidermal growth factor (EGF)-like domain binds calcium. High  
 resolution NMR structure of the calcium form of the NH2-terminal EGF-  
 like domain in coagulation factor X";  
 J. Biol. Chem. 267:19642-19649 (1992).  
 [13] J. Biol. Chem. 267:19642-19649 (1992).  
 STRUCTURE BY NMR OF 41-126.  
 MEDLINE=96387194; PubMed=8794734;  
 Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,  
 Trewella J.;  
 "The relative orientation of Gla and EGF domains in coagulation  
 factor X is altered by Ca2+ binding to the first EGF domain. A  
 combined NMR-small angle X-ray scattering study.";  
 Biochemistry 35:11547-11559 (1996).  
 -!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 converts prothrombin to thrombin in the presence of factor Va,  
 calcium and phospholipid during blood clotting.  
 -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-(I-Thr and then  
 Arg-I-Ile bonds in prothrombin to form thrombin.  
 -!- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 AFTER THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 MORE DISULFIDE BONDS.  
 -!- TM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CALCIUM.  
 -!- PTM: N- AND O-GLYCOSYLATED.  
 -!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 -!- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 -!- SIMILARITY: Contains 2 EGF-like domains.  
 -----  
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 EMBL X00673; CAA25286.1; -;  
 PIR: A22867; EXBO.  
 DR PDB: 1APO; 31-JAN-94.  
 DR PDB: 1CCF; 31-MAY-94.  
 DR PDB: 1WHE; 15-MAY-97.  
 DR PDB: 1WHF; 15-MAY-97.  
 DR PDB: 1IOD; 21-JAN-03.  
 DR PDB: 1KIG; 28-OCT-98.  
 DR MEROFS; S01.216; -;  
 GlycoSuiteDB: P00743; -;  
 DR

FT MOD\_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID (BY  
SIMILARITY).  
FT MOD\_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY  
SIMILARITY).  
FT MOD\_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY  
SIMILARITY).  
FT MOD\_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY  
SIMILARITY).  
FT MOD\_RES 103 103 HYDROXYLATION (BY SIMILARITY).  
FT ACT\_SITE 274 274 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 320 320 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 417 417 CHARGE RELAY SYSTEM.  
FT DISUFD 90 101 BY SIMILARITY.  
FT DISUFD 95 110 BY SIMILARITY.  
FT DISUFD 112 121 BY SIMILARITY.  
FT DISUFD 129 140 BY SIMILARITY.  
FT DISUFD 136 149 BY SIMILARITY.  
FT DISUFD 151 164 BY SIMILARITY.  
FT DISUFD 172 340 INTERCHAIN (BY SIMILARITY).  
FT DISUFD 239 244 BY SIMILARITY.  
FT DISUFD 259 275 BY SIMILARITY.  
FT DISUFD 388 402 BY SIMILARITY.  
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 490 AA; 53965 MW; 3A39FA85AF2A6D11 CRC64;

Query Match 74.0%; Score 1949; DB 1; Length 490;  
Best Local Similarity 74.8%; Pred. No. 6.1e-134;  
Matches 356; Conservative 50; Mismatches 68; Indels 2; Gaps 1;

QY 1 MGRPLHLVLSASLAGLLLGESLFIREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
D 1 MANPLHLVLLGAALAGLLSGSVFISRAANDVLARTTRANSFLEELKKGHLERECMEE 60  
QY 61 TCSYEAREVFEFSDKTFNEFNWYKDGQCEPQNGCKDGLGYETCTCLEGEGKN 120  
D 61 NCSYEAREVFEFDEKTFNEFNWYKDGQCESNPQNGCKDGLGYETCTCLEGEGQD 120  
QY 121 CELTRKCLSDNGDQDFCHEQNSVVCARGYTLADNGKACIPTPGPGKQTLERR 180  
D 121 CEPVTRKCLSDNGDQDFCKEENSVLSCASSYTLGDKGKSCISTELFPCKGVTLGRW 180  
QY 181 KRSVAQATSSGEAPDSITWPKYDAADLDPTENPFDLLDNQTPQPERGNNLFRIVGGQE 240  
D 181 RRS--PATNSSEGPPEAPGPEQDDGNLTATENPFLNLSPEPPEDSSSLRIVGGQD 238  
QY 241 CKDGECPQALLINEEGFCGGTILSEFVILTAACHLYOAKRFKVRVGDNRNTEQEGGE 300  
D 239 CROGECPOALLNEEGFCGGTILSEYHLVLAACHLYOAKRFKVRVGDNRDTEHEEGNE 298  
QY 301 AVHEVEVVIKHNFTKETYDFDIAVLRLKTPITFRMNVPACILPERDWAESTLMTQGTI 360  
D 299 ETHEVEVVVHNFRVFKETYDFDIAVLRLKTPITFRMNVPACILPERDWAESTLMTQGTI 358  
QY 361 VSGFGRTHKROSTRLKMLEVPYVDRNSKLLSSFIITQNMFCAGYDTKQEDACGDSG 420  
D 359 VSGFGRTHKROSTRLKMLEVPYVDRNSKLLSSFIITQNMFCAGYDARPEACGDSG 418  
QY 421 GPHVTRFKDTFYFTGVISWEGSCARKGKYGIYTKVTAFLKWDKSMKTRGLPKAKS 476  
D 419 GPHVTRFKDTFYFTGVISWEGSCARKGKYGIYTKVTAFLKWDKSMKTRGLPKAKS 474

RESULT 3  
FA10\_BOVIN  
ID FA10\_BOVIN STANDARD; PRT; 492 AA.  
AC P00743;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-ANG-1987 (Rel. 05, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).

GN F10.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE OF 1-487 FROM N.A.  
RX MEDLINE=84247315; PubMed=6330671;  
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;  
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain  
RL containing a prepro leader sequence.";  
RN Nucleic Acids Res. 12:4481-4492(1984).  
[2]  
RP SEQUENCE OF 41-180.  
RX MEDLINE=80130563; PubMed=6766735;  
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,  
RA Titani K.;  
RT "Amino acid sequence of the light chain of bovine factor X1 (Stuart  
RL factor).";  
RN Biochemistry 19:659-667(1980).  
[3]  
RP REVISION TO 103.  
RX MEDLINE=83308813; PubMed=6688526;  
RA McMullen B.A., Fujikawa K., Kisiel W.;  
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
RL K-dependent blood coagulation zymogens.";  
RN Biochem. Biophys. Res. Commun. 115:8-14(1983).  
[4]  
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
RX MEDLINE=76053069; PubMed=1059093;  
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,  
RA Neurath H.;  
RT "Bovine factor X1 (Stuart factor): amino-acid sequence of heavy  
RL chain.";  
RN Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).  
[5]  
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=94062825; PubMed=8243461;  
RA Inoue K., Morita T.;  
RT "Identification of O-linked oligosaccharide chains in the activation  
RL peptides of blood coagulation factor X. The role of the carbohydrate  
RN moieties in the activation of factor X.";  
RX Eur. J. Biochem. 218:153-163(1993).  
[6]  
RP ACTIVE SITE.  
RX MEDLINE=73053314; PubMed=4264286;  
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,  
RA Neurath H., Davie E.W.;  
RT "Bovine factor X1a (activated Stuart factor). Evidence of homology  
RL with mammalian serine proteases.";  
RN Biochemistry 11:4899-4903(1972).  
[7]  
RP PROCESSING.  
RX MEDLINE=76053121; PubMed=1059122;  
RA Fujikawa K., Titani K., Davie E.W.;  
RT "Activation of bovine factor X (Stuart factor): conversion of factor  
RN Xa-alpha to factor Xa-beta.";  
RX Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).  
[8]  
RP CALCIUM-BINDING DATA.  
RX MEDLINE=84185716; PubMed=6546930;  
RA Sugo T., Björk I., Holmgren A., Stenflo J.;  
RT "Calcium-binding properties of bovine factor X lacking the gamma-  
RN carboxylglutamic acid-containing region.";  
RX J. Biol. Chem. 259:5705-5710(1984).  
[9]  
RP SULFATON.  
RX MEDLINE=86140210; PubMed=3949800;  
RA Morita T., Jackson C.M.;  
RT "Localization of the structural difference between bovine blood  
RN coagulation factors X1 and X2 to tyrosine 18 in the activation  
RT peptide.";

Query Match	99.88	Score 2630	DB 1	Length 488
Best Local Similarity	99.88	Pred. No. 3e-183		
Matches 487	Conservative	0	Mismatches	1
		0	Indels	0
		0	Gaps	0
1	MGRPLHLVLLSASLAGLLLGESLFI	IRREQANNILARVTRANSFL	EMKKGHLERECMEE	60
1	MGRPLHLVLLSASLAGLLLGESLFI	IRREQANNILARVTRANSFL	EMKKGHLERECMEE	60
61	TCSEEARVFEVSDKTNFVWNYK	KGDCQETSPCQNOGCKDGLGEY	TCTCLEGFEKN	120
61	TCSEEARVFEVSDKTNFVWNYK	KGDCQETSPCQNOGCKDGLGEY	TCTCLEGFEKN	120
121	CELFTRKLCSLDNGDCDQFCH	EEQNSVVCSCARGYTLADNGK	ACIPTGPPCGKQTLERR	180
121	CELFTRKLCSLDNGDCDQFCH	EEQNSVVCSCARGYTLADNGK	ACIPTGPPCGKQTLERR	180
181	KRSVAQATSSSGEAPDSITWK	PYDAADLDPENPFLLDNQTP	QPERGDNLTIRIVGGQE	240
181	KRSVAQATSSSGEAPDSITWK	PYDAADLDPENPFLLDNQTP	QPERGDNLTIRIVGGQE	240
241	CKDGECPWQALLINEEGFCGG	TILSEFVILTAACHLYQAKRF	KVVRGDRNTEQEEGGE	300
241	CKDGECPWQALLINEEGFCGG	TILSEFVILTAACHLYQAKRF	KVVRGDRNTEQEEGGE	300
301	AVHEVYVVIKHNRTKETYPD	FIADVLRLKTIPTFRMNVPA	CPALPERDWAESTLMTQGT	360
301	AVHEVYVVIKHNRTKETYPD	FIADVLRLKTIPTFRMNVPA	CPALPERDWAESTLMTQGT	360
361	VSGFRGTHEKGROSTRUKL	MEVPPVDRNSCKLSSFTI	TONMFCAGYDKOEDACOGDSG	420
361	VSGFRGTHEKGROSTRUKL	MEVPPVDRNSCKLSSFTI	TONMFCAGYDKOEDACOGDSG	420
421	GPVHTREKDTYFVGI	SWGESCARKGYGIYTKVTA	FLKWIIDRSMKTRGLPKAKSHAPE	480
421	GPVHTREKDTYFVGI	SWGESCARKGYGIYTKVTA	FLKWIIDRSMKTRGLPKAKSHAPE	480
481	VITSSPLK 488			
481	VITSSPLK 488			
RESULT 2				
FA10_RABIT	STANDARD;	PRF;	490 AA.	
AC	O1905			
DT	15-DEC-1998	(Rel. 37, Created)		
DT	15-DEC-1998	(Rel. 37, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DT	Coagulation factor X precursor	(EC 3.4.21.6) (Stuart factor).		
GN	F10			
OC	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI TaxID=9986;			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=97256311; PubMed=9101642;			
RX	Pendurthi U.R., Anderson K.D., James H.L.;			
RT	"Characterization of a full-length cDNA for rabbit factor X.;"			
RL	Thromb. Res. 85:503-514 (1997).			
CC	-1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.			
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Thr and then Arg- -Ile bonds in prothrombin to form thrombin.			
CC	-1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.			
CC	-1- TM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).			
CC	-1- STM: N- AND O-GLYCOSYLATED (BY SIMILARITY).			

RL Biochemistry 22:2875-2884(1983).  
 RP [7]  
 RN  
 RC SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Levis S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X";  
 RL Proc Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RN [8]  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [9]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagasevaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X";  
 RL Gene 84:517-519(1989).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=835279;  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";   
 RL J. Mol. Biol. 232:947-966(1993).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa";  
 RL Proc Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 RN [12]  
 RP VARIANTS ILE-7 AND HIS-30.  
 RX MEDLINE=99318093; PubMed=10391209;  
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Landry E.S.;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes";  
 RL Nat. Genet. 22:231-238(1999).  
 RN [13]  
 RP ERRATUM.  
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Landry E.S.;  
 RL Nat. Genet. 23:373-373(1999).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- TM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- TM: N- AND O-GLYCOSYLATED.  
 CC -1- TM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC DR EMBL; K01194; AAA52490.1; -  
 CC DR EMBL; M57285; AAA52421.1; -  
 CC DR EMBL; AF503510; AAM19347.1; -  
 CC DR EMBL; L29433; AAA52764.1; -  
 CC DR EMBL; L00390; AAA52764.1; JOINED.  
 CC DR EMBL; L00391; AAA52764.1; JOINED.  
 CC DR EMBL; L00392; AAA52764.1; JOINED.  
 CC DR EMBL; L00393; AAA52764.1; JOINED.  
 CC DR EMBL; L00394; AAA52764.1; JOINED.  
 CC DR EMBL; L00395; AAA52764.1; JOINED.  
 CC DR EMBL; L00396; AAA52764.1; JOINED.  
 CC DR EMBL; M22613; AAA51984.1; -  
 CC DR EMBL; K01886; AAA52486.1; -  
 CC DR EMBL; M33297; AAA52636.1; -  
 CC DR EMBL; A24478; EXHU. -  
 CC DR PDB; 1HCG; 08-MAY-95.  
 CC DR PDB; 1FAX; 29-OCT-97.  
 CC DR PDB; 1FXV; 17-JUN-98.  
 CC DR PDB; 1XKA; 23-MAR-99.  
 CC DR PDB; 1XKB; 23-MAR-99.  
 CC DR PDB; 1EQO; 20-SEP-00.  
 CC DR PDB; 1FOR; 20-SEP-00.  
 CC DR PDB; 1FOS; 20-SEP-00.  
 CC DR PDB; 1FJS; 17-NOV-00.  
 CC DR PDB; 1G2L; 20-OCT-01.  
 CC DR PDB; 1G2M; 20-OCT-01.  
 CC DR PDB; 1KSN; 19-JUN-02.  
 CC DR PDB; 1KVE; 11-FEB-03.  
 CC DR PDB; 1MQ5; 28-JAN-03.  
 CC DR PDB; 1MQ6; 28-JAN-03.  
 CC DR PDB; 1NFU; 25-FEB-03.  
 CC DR PDB; 1NFW; 25-FEB-03.  
 CC DR PDB; 1NFX; 25-FEB-03.  
 CC DR PDB; 1NFX; 25-FEB-03.  
 CC DR MEROPS; S01.216; -  
 CC DR GlycoSuiteDB; P00742; -  
 CC DR Genew; HGNC:3528; F10.  
 CC DR MIM; 134530; -  
 CC DR MIM; 227600; -  
 CC DR GO; GO:0005576; C:extracellular; TAS.  
 CC DR GO; GO:0003804; F:blood coagulation factor X activity; TAS.  
 CC DR GO; GO:0007596; P:blood coagulation; TAS.  
 CC DR InterPro; IPR000152; Asx\_hydroxyl.  
 CC DR InterPro; IPR001314; Chymotrypsin.  
 CC DR InterPro; IPR000742; EGF\_2.  
 CC DR InterPro; IPR001881; EGF\_Ca.  
 CC DR InterPro; IPR001438; EGF\_II.  
 CC DR InterPro; IPR006209; EGF\_like.  
 CC DR InterPro; IPR002383; GLA\_blood.  
 CC DR InterPro; IPR001254; Ser\_protease\_Try.  
 CC DR Pfam; PF00008; EGF; 2.  
 CC DR Pfam; PF00594; gla; 1.  
 CC DR Pfam; PF00089; trypsin; 1.  
 CC DR PRINTS; PR00722; CHYMOTRYPSIN.  
 CC DR PRINTS; PR00010; EGFBLD.  
 CC DR PRINTS; PR00001; GLABLOOD.  
 CC DR SMART; SM00179; EGF\_CA; 1.  
 CC DR SMART; SM00069; GLA; 1.  
 CC DR SMART; SM00020; Tryp\_SPC; 1.  
 CC DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC DR PROSITE; PS00022; EGF\_1; 1.  
 CC DR PROSITE; PS01186; EGF\_2; 2.  
 CC DR PROSITE; PS01187; EGF\_CA; 1.  
 CC DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 CC DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on:

August 11, 2003, 10:16:54 ; Search time 26 Seconds  
(without alignments)  
882.655 Million cell updates/sec

Title: US-09-632-722-2

Perfect score: 2634

Sequence: 1 MGRPLHLVLLSASLAGLLLL.....RGLPKAKSHAPVITSSPLK 488

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database

SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	2630	99.8	488	1	FA10_HUMAN	P00742 homo sapien
2	1949	74.0	490	1	FA10_RABIT	O39045 oryctolagus
3	1851	70.3	492	1	FA10_BOVIN	P00743 bos taurus
4	1425	54.1	475	1	FA10_CHICK	P25155 gallus gall
5	1135.5	43.1	376	1	FA10_TROCA	P81428 tropidechis
6	1041.5	39.5	461	1	FA9_HUMAN	P00740 homo sapien
7	1039.5	38.5	459	1	FA9_MOUSE	P16294 mus musculus
8	1032.5	39.2	452	1	FA9_CANFA	P19540 canis famul
9	963	36.6	416	1	FA9_BOVIN	P00741 bos taurus
10	954	36.2	444	1	FA7_RABIT	P88139 oryctolagus
11	948	36.0	466	1	FA7_MOUSE	P08709 homo sapien
12	909.5	34.5	446	1	FA7_MOUSE	P70375 mus musculus
13	872	33.1	407	1	FA7_BOVIN	P22457 bos taurus
14	872	33.1	456	1	PRTC_BOVIN	P00745 bos taurus
15	861	32.7	461	1	PRTC_RAT	P31394 rattus norv
16	858	32.6	461	1	PRTC_MOUSE	P33587 mus musculus
17	853.5	32.4	459	1	PRTC_PIG	Q9gip2 sus scrofa
18	829.5	31.5	458	1	PRTC_RABIT	Q28661 oryctolagus
19	827	31.4	461	1	PRTC_HUMAN	P04070 homo sapien
20	837	24.2	622	1	THRB_HUMAN	P19221 mus musculus
21	821.5	23.6	618	1	THRB_MOUSE	P00735 bos taurus
22	598.5	22.7	625	1	THRB_BOVIN	P22891 homo sapien
23	594.5	22.6	617	1	THRB_RAT	P16292 rattus norv
24	585.5	22.2	400	1	PRTZ_HUMAN	P16292 oryctolagus
25	568	21.6	275	1	FA9_RABIT	P16296 rattus norv
26	566	21.5	282	1	FA9_RAT	P16296 cavia porce
27	559.5	21.2	285	1	FA9_CAVPO	P16295 mus musculus
28	544.5	20.7	271	1	FA9_PIG	P16293 sus scrofa
29	521	19.8	274	1	FA9_SHEEP	P16291 ovis aries
30	510	19.4	396	1	PRTZ_BOVIN	P00744 bos taurus
31	417	15.8	562	1	TPA_HUMAN	P00750 homo sapien
32	15.5	15.8	247	1	TRY4_RAT	P12788 rattus norv
33	415	15.8	559	1	TPA_RAT	P19637 rattus norv

## RESULT 1

ID	FA10_HUMAN	STANDARD;	PRT;	488 AA.
AC	P00742; Q14340;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).			
GN	F10.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91216473; PubMed=1902434;			
RA	Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;			
RT	"Cloning and expression in COS-1 cells of a full-length cDNA encoding			
RT	human coagulation factor X.";			
RL	Gene 99:291-294(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87026600; PubMed=3768336;			
RA	Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;			
RT	"Gene for human factor X: a blood coagulation factor whose gene			
RT	organization is essentially identical with that of factor IX and			
RT	protein C.";			
RL	Biochemistry 25:5098-5102(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,			
RA	Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;			
RT	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE OF 13-488 FROM N.A.			
RX	MEDLINE=85216545; PubMed=2582420;			
RA	Fung M.R., Hay C.W., McGillivray R.T.A.;			
RT	"Characterization of an almost full-length cDNA coding for human			
RT	blood coagulation factor X.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).			
RN	[5]			
RP	SEQUENCE OF 19-488 FROM N.A.			
RA	TISSUE=Liver;			
RX	MEDLINE=86221713; PubMed=3011603;			
RA	Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;			
RT	"Isolation and characterization of human blood-coagulation factor X			
RT	cDNA.";			
RL	Gene 41:311-314(1986).			
RN	[6]			
RP	SEQUENCE OF 41-179.			
RX	MEDLINE=83257207; PubMed=6871167;			
RA	McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,			
RA	Kwa E.Y., Weinstein B.;			
RT	"Complete amino acid sequence of the light chain of human blood			
RT	coagulation factor X: evidence for identification of residue 63 as			
RT	beta-hydroxyaspartic acid.";			

## ALIGNMENTS

34	413	15.7	559	1	TPA_MOUSE	P11214 mus musculus
35	412	15.6	247	1	TRY3_RAT	P08426 rattus norv
36	404	15.3	686	1	MAS2_HUMAN	O00187 homo sapien
37	402.5	15.3	477	1	URT2_DESRO	P15638 desmodus ro
38	401.5	15.2	434	1	URCK_CHICK	P15120 gallus gall
39	396	15.0	566	1	TPA_BOVIN	Q28198 bos taurus
40	396	15.0	638	1	KAL_RAT	P14272 rattus norv
41	394.5	15.0	231	1	TRY2_SALSA	P35032 salmo salar
42	392	14.9	855	1	ST14_MOUSE	Q9er04 mus musculus
43	391.5	14.9	455	1	TMS5_MOUSE	P35030 homo sapien
44	391	14.8	304	1	TRY3_HUMAN	P35038 anopheles g
45	389.5	14.8	275	1	TRY4_ANOGA	

Eur. J. Haematol. 52, 162-168, 1994  
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of  
A:Reference number: I46196; MUID:94222160; PMID:8168596  
A:Accession: I62744  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-161 <RES>  
A:Cross-references: GB:D21214; MID:9415307; PIDN:BA04755.1; PID:g455395  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate  
F:1-161/Domain: trypsin homology (fragment) <TRY>

Query Match 31.8%; Score 837; DB 2; Length 161;  
Best Local Similarity 96.9%; Pred. No. 2.4e-50;  
Matches 156; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 297 EGGEAVHEVVIKHNRTKETFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQ 356  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 EGGEAVHEVVIKHNRTKETFDIAVLRLKSPITFRMNVAPACLPERDWAESTLMTQ 60  
QY 357 KTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKLSSFFITQNMFCAGYDTKQEDACQ 416  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
61 KTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKLSSFFITQNMFCAGYHAKQEDACQ 120  
QY 417 GDSGGPHVTRFKDTYFVTGIVSWGESCARKKGYIYTKVTA 457  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
121 GDSGGPHVTRFKDTYFVTGIVSWGESCARKKGYIYTKVTA 161

Search completed: August 11, 2003, 10:27:30  
Job time 43 secs

A:Accession: S24312  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <OKA2>

A:Cross-References: EMBL:X64336; NID:g55962; PIDN:CA45617.1; PID:g55963  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:27-85/Domain: Gla domain homology <GLA>  
 F:33-42/Domain: propeptide #status predicted <PRO>  
 F:43-461/Product: protein C #status predicted <PRC>  
 F:91-130/Domain: EGF homology <EG1>  
 F:139-174/Domain: EGF homology <EG2>  
 F:213-445/Domain: trypsin homology <TRY>  
 F:47, 48, 57, 60, 61, 66, 67, 70, 76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130, 139-150, 146-159, 161-174, 182-320, 339-255, 373-387, 398-426/Disulfide bonds: #stat  
 F:215, 291, 355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:254, 300, 402/Active site: His, Asp, Ser #status predicted

Query Match 32.7%; Score 861; DB 1; Length 461;

Best Local Similarity 36.4%; Pred. No. 1.7e-51;  
 Matches 182; Conservative 81; Mismatches 159; Indels 78; Gaps 11;

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7 LVLSA---LAGLLLGESLIRREQANNILARVTRANSFLREEMKKHGLERECMEETCS 63
8 IFLFASTWGISGSAHPDPVFSSEGAHQVL-RVRANSFLFEEVRAGSLERECMEICD 64
64 YEAREVFESDKTNEFNWYKDGQDET-----SPQNGCKKDGGLGYETCTCLEG 115
65 FEEAEIFQNVEDTLAFWIKYFDGQDCSTPLDHCQDSPCCGHGTCIDGLGFGSCDKG 124
116 FEGKNCLEFTRK---CSLDNGDCDQCFHEEQNSVVCARGYTLADNGKACIPGYP 171
125 WEGFQC--QEMFGQDCRVKNGGCHYCLEETRGRCRCAPGYELADDMHCRPTVNP 181
172 CGKOTLERRKRSVAQATSSSGEAPDSITWKPYD-----AADLPTENPFDLLDFNQTP 225
182 CGK-----LWKRTDKRKNFRDIDPEDELEL-----209
226 ERGDNLTIRVGOECKDCECPNQALLINEENEGFCGTTILSEFYILTAHCLYQAKR 285
210 -----GPRVINGTLTKQGDSPWQAILLDSKKLACGGVLIHTSWLTAHCLLESSK 263
286 VRVGDRTVEEGEAEVHEVVIKHNFTKETYDFDIAVLRLKTPITFRMNVPACLP 345
264 VRGEYDLRRDPEWLDLKEILVHPNTRSSNDIALRLSQATLSKTIPIVCLN 323
346 RMAESTLMTQKTGIYSGVGFRTHEKGRQSTR-----LKMLEVYVDNRNSCKLS 400
324 SGLAQELSAQGETVVTWGYQSDKVKDGRNRTFILTIRIPLAARNDCMVMNNVWSE 383
401 NMFCAGYDTQEDACQDGGPHVTFKDYFTVGTIVSGWSCARCKGYIKTKVTAFLK 460
384 NMLCAGITGTRDAGDGGPMVVFRTGTFWLVGLVSGEGCGHNNYGVTKVGSYLK 443
461 WI-----DRSMKTRGLPK 473
444 WIHSYIGERDVSLKS-----PK 460

```

RESULT 14  
 JX0210

protein C (activated) (EC 3.4.21.6) precursor - mouse  
 N:Alternate names: vitamin K-dependent serine proteinase  
 C:Species: Mus musculus (house mouse)  
 C:Date: 1-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
 C:Accession: JX0210  
 J:R. Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.  
 J:Biochem 111, 491-495, 1992  
 A:Title: Isolation and characterization of a mouse protein C cDNA.  
 A:Reference number: JX0210; MUID:92316897; PMID:1618739  
 A:Accession: JX0210

A:Molecule type: mRNA  
 A:Residues: 1-461 <TAD>

A:Cross-References: GB:D10445; NID:g220385; PIDN:BA01235.1; PID:g220386  
 A:Experimental source: liver  
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that

s.  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu  
 F:1-33/Domain: signal sequence #status predicted <SIG>  
 F:27-85/Domain: Gla domain homology <GLA>  
 F:34-41/Domain: propeptide #status predicted <PRO>  
 F:42-196, 199-461/Product: protein C #status predicted <PRC>  
 F:42-196/Domain: light chain #status predicted <PCL>  
 F:91-130/Domain: EGF homology <EG1>  
 F:139-174/Domain: EGF homology <EG2>  
 F:199-461/Domain: heavy chain #status predicted <PCH>  
 F:199-211/Domain: activation peptide #status predicted <ACT>  
 F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>  
 F:212-445/Domain: trypsin homology <TRY>  
 F:47, 48, 55, 57, 60, 61, 66, 67, 70, 76/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:121-130, 139-150, 146-159, 161-174, 182-319, 238-254, 373-387, 398-426/Disulfide bonds: #s  
 F:214, 290, 355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:253, 299, 402/Active site: His, Asp, Ser #status predicted

Query Match 32.6%; Score 858; DB 1; Length 461;

Best Local Similarity 37.0%; Pred. No. 2.8e-51;  
 Matches 179; Conservative 88; Mismatches 161; Indels 56; Gaps 10;

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7 LVLSA-SIAGLLLGESLIRREQANNILARVTRANSFLREEMKKHGLERECMEETCSYE 65
8 LLLMTGWISGSAHPDPVFSSEGAHQVL-RVRANSFLFEEVRAGSLERECMEICD 66
66 YEAREVFESDKTNEFNWYKDGQDET-----SPQNGCKKDGGLGYETCTCLEGE 117
67 EAEIIFQNVEDTLAFWIKYFDGQCSAPPLDHCQDSPCCGHGTCIDGIFSGSCDKGWE 126
118 GKNCLEFTR-KLCSLDNGDCDQCFHEEQNSVVCARGYTLADNGKACIPGYPGK-- 174
127 GKFCQQLRFQDCRVNNGGCHYCLEESNRRRCACAPGYELADDMHCRKSTVNPFCGLG 186
175 QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLPTENPFDLLDFNQTPERGNL 234
187 RWIEKKRKLTKRDT-----DLELEFPD-----R 211
235 IVGGOECKDCECPNQALLINEENEGFCGTTILSEFYILTAHCLYQAKRKYRVGDRNTE 294
212 IVNGTLTKQGDSPWQAILLDSKKLACGGVLIHTSWLTAHCVGTRKLVRLGEYDLR 271
295 QEEGGEAEVHEVVIKHNFTKETYDFDIAVLRLKTPITFRMNVPACLPEDWA--EST 352
272 RDHWELDLDIKEILVHPNTRSSNDIALRLAQATLSKTIPIVCLPNNGLAQBELT 331
353 LMTQKTGIYSGVGRTHKGRQSTR-----LKMLEVYVDNRNSCKLSSEFITTQMFCA 407
332 QAGQET-VVTWGYQSDRIKDGRRNRTFILTIRIPLVARNECEVEMNNVSNMLCAGI 390
408 DTKQEDACQDGGPHVTFKDYFTVGTIVSGWSCARCKGYIKTKVTAFLKIDRSMK 467
391 IGNTRDACDGGSGPMVVFRTGTFWLVGLVSGEGCGHNNYGVTKVSYLKHVHISIG 450
468 TRGL 471
451 EKG 454

```

RESULT 15  
 I62744

coagulation factor Xa (EC 3.4.21.6) - rhesus macaque (fragment)  
 C:Species: Macaca mulatta (rhesus macaque)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 22-Jun-1999  
 C:Accession: I62744  
 R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.



[illegible]

## RESULT 12

protein C(activated) (EC 3.4.21.69) precursor - bovine (fragment)  
N:Alternate names: autoprothrombin IIA; plasma protein C  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 30-Nov-1980 #sequence-revision 17-Mar-1987 #text\_change 16-Jul-1999  
C:Accession: A26250; A18385; A18386; A00928  
R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984  
A:A>Title: Cloning and sequence of liver cDNA coding for bovine protein C.  
A:A:Reference number: A26250; MUID:85014826; PMID:6091100  
A:C:Accession: A26250  
A:Molecule type: mRNA  
A:Residues: 1-456 <LONG>  
J.R.Fernlund, P.; Stenflo, J.  
J. Biol. Chem. 257, 12170-12179, 1982  
A:A>Title: Amino acid sequence of the light chain of bovine protein C.  
A:A:Reference number: A18385; MUID:83007325; PMID:6896876  
A:C:Accession: A18385  
A:Molecule type: protein  
A:Residues: 40-194 <FER>  
A:A>Note: 81-Lys was also found  
R.R.Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.  
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983  
A:A>Title: Beta-Hydroxyaspartic acid in vitamin K-dependent protein C.  
A:A:Reference number: A19316; MUID:83169769; PMID:6572939  
A:A:Contents: annotation; revision to residue 110  
R.R.Stenflo, J.; Fernlund, P.  
J. Biol. Chem. 257, 12180-12190, 1982  
A:A>Title: Amino acid sequence of the heavy chain of bovine protein C.  
A:A:Reference number: A18386; MUID:83007326; PMID:6896877  
A:C:Accession: A18386  
A:Molecule type: protein  
A:Residues: 197-454, 'PV' <STE>  
R.R.Esmon, N.L.; DeBault, L.E.; Esmon, C.T.  
J. Biol. Chem. 258, 5548-5553, 1983  
A:A>Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F  
A:A:Reference number: A37541; MUID:83213513; PMID:6304092  
A:A:Contents: annotation; activation; calcium binding  
J.R.Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.  
J. Biol. Chem. 258, 5554-5560, 1983  
A:A>Title: Structural changes required for activation of protein C are induced by Ca<sup>2+</sup> bin  
A:A:Reference number: A37542; MUID:83213514; PMID:6406503  
A:A:Contents: annotation; activation; calcium binding  
Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re  
Comment: Protein C is synthesized in the liver as a single chain precursor, which is o  
chain, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti  
Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str  
Recognition of the thrombin-thrombomodulin complex.  
Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin  
Comment: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
Superfamily:

C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind  
F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>  
F;24-83/Domain: Gla domain homology <GLA>  
F;30-39/Domain: propeptide #status predicted <PRO>  
F;40-194/Product: protein C light chain #status experimental <LCH>  
F;98-128/Domain: EGF homology <EGI>  
F;137-172/Domain: EGF homology <EG2>  
F;197-456/Product: protein C heavy chain #status experimental <HCH>  
F;197-210/Domain: activation peptide #status experimental <APT>  
F;211-440/Domain: trypsin homology <TRY>  
F;45-46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #s  
F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #s  
F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;252,298,397/Active site: His, Asp, Ser #status predicted  
F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.1%; Score 872; DB 1; Length 456;  
Best Local Similarity 38.7%; Pred. No. 3e-52;  
Matches 183; Conservative 83; Mismatches 155; Indels 52; Gaps 10;

QY 22 ESILTRREQANNILARVTRANSFLIEMKKGHLERECMETCSYEAREVFEDSDKTNEPW 81  
Db :  
21 DSVFSSQRAHQVLIRKRANSFLBELRPGNVRECESEVEFEAREIFQNTDMAFW 80  
QY 82 NKYKDGDQCETS-----PQNQGCKDGLGEYTCTCLEGFEGKNCELFR-KLCSLD 132  
Db :  
81 SFYSDGDQCEDRPSPGCDLPCCGRGKCIDGLGGFRCDCAEGWGRCFLHEVRFNSCNAE 140  
QY 133 NGDCDOFHCEEQNSVVCARGYTLADNGKACIPTGPYCGK--OTLBERRKRSVAQAATSS 190  
Db :  
141 NGGCACHYCMEEGRHCSCAPGYREDHDQLCVSKVTFPCGRLGRMEKKRTLRDTNQ 200  
QY 191 SGEAPDSITWKPYDAAD-LDPTEPNFDLLDFNQTPERGDNNLTRIVGOECKGCECPWQ 249  
Db :  
201 -----VDQKDLDP-----RIVDQQAGMGESPWQ 225  
QY 250 ALLINEENEGFGGTILSEFYILTAAHCLYQAKRKFKVRGDRNTEQEGBGVHEVEYVI 309  
Db :  
226 AVLLDSKKLLCVGAVLIHVSWLTVAHCLDSRKKLIVRLGEYDMRRWSWEVDLDIKEVI 285  
QY 310 KHNRTKETTYDFDI AVLRLKPTIFRMNVAPACIPERDWAS--TLMQTGTVSGGFFT 367  
Db :  
286 IHPNYTKTSNDIALLAKPATLSQTVICIPDLSGLSERKLTQVGQET-VVTGWGYR 344  
QY 368 HEKGRQST-RLKMLEVPVYDRNSCKLSSFIITQMFCAGYDTKQEDACQDSGGPHVTR 426  
Db :  
345 DETKRNRTFVLISIKVPVYNACVHAMENKISENMLCAGILGDPDACEGSDSGPWNVTF 404  
QY 427 FKDYIFYTGIVSWEASCARKKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP 479  
Db :  
405 FRGTWFLGLVSWGEGCRLYNGYVTKVSRYLDWIYGHKAQEAPE-LESQVP 456

RESULT 13  
SI18994.

protein C (activated) (EC 3.4.21.69) precursor - rat  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Oct-1999  
C.Accession: SI18994; S24312  
Submitted by: T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
submitted to the EMBL Data Library, February 1992  
A.Submission: The cDNA cloning and mRNA expression of rat protein C.

RESULT 13

SI8994. protein C (activated) (EC 3.4.21.69) precursor - rat  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Oct-1999  
C.Accession: SI8994; S24312  
C.R:R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
A.Description: The cDNA cloning and mRNA expression of rat protein C.  
A.Reference number: SI8994  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-461 <OKA>  
A.Cross-references: EMBL:X64336; NID:g56962; PID:CAA45617.1; PID:g56963  
R:R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.  
Biochim. Biophys. Acta 1131, 329-332, 1992  
Title: The cDNA cloning and mRNA expression of rat protein C.  
Reference number: S24312; MUID:92329550; PMID:1627650

180 LIADGVSCTPTVEYPCGKIPILKRNASPGQ----- 211  
216 DLLDFNQOTPERGNNLIRIVGQEGCKGECQWQALLINEENEGFCGGTILSEFYILTA 275  
212 -----RIVGKVKPCGECQWQVLL-VNGAQLCGGTILINTIIVWSAA 252  
276 HCLYQAKRFK---VRVGRNTEQEGEAVHEVEVVKINRFTKTYDFEDIAVLKTLPL 332  
253 HCFDKIKNWNRLIAVLGEHDLSDHDEQSRRAQVIIPSTVYVPGTNDHIALLRHQPV 312  
333 TFRMNVAPACLPDRAEASTLMTQKTVGSGFQRTHEKGRQSLKMLNLEVPVYDRNSC-- 390  
313 VLTDHVVPLCLPRTSERTLAFVRSLSVSGWQLLDGATALEMLVNLVPRMTDCLQ 372  
391 ---KLSSFTIITQMFACGYDTKQEDACQDGGPHTVRFKDYFTVGTIVSGESCARG 447  
373 QSRKVGSPNITEYMFACGYSDGSKDCKGSGPHATHYRGWYLTGIVSGQGCATVG 432  
448 KYGIYKVTAFWLKIDRSMKTRGLPKAKSHAP 479  
433 HFGVYTRVSYIEMLOKMRSEPRPGVLLRAP 464

RESULT 10  
146932  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 0-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 12-Feb-1999  
C:Accession: I46932  
R:Brother, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.  
Thromb. Res. 69, 231-238, 1993  
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII  
A:Reference number: I46932; MUID:93190306; PMID:8383365  
A:Accession: I46932  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-443 <BRO>  
A:Cross-references: GB:856300; NID:g266294; PID:g266295  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
F:124-83/Domain: Gla domain homology <GLA>  
F:189-120/Domain: EGF homology <EGF>  
F:130-166/Domain: EGF homology <EG2>  
F:192-425/Domain: trypsin homology <TRY>

Query Match 35.9%; Score 945.5; DB 2; Length 443;  
Best Local Similarity 40.6%; Pred. No. 2.8e-57;  
Matches 193; Conservative 73; Mismatches 142; Indels 67; Gaps 9;

7 LVLLSASLAGLLLGESLFTIRREOANNILARVTRANSFLEMKKGLHLEKMEETCSYEE 66  
13 LLALQASLA-----AVFITQEEAHSVLRQRANSFLELRPSGLERECKELCSFEE 65  
67 AREVPFSDKTNFENYKDKDQCTSPCQNGCKDGLGEYTCCTLEGEGKNCE--LF 124  
66 AREVPQSTERTKFWITNDGQASNPQNGSGCEDQIQSYITCFCLADFEGRNCKNKN 125  
125 TRKLCSLDNGDQDFCHEEQNSV-VCSARGYTLADNGKACIPGPGK-QTLERRKR 182  
126 DOLICMYENGCEQYCSHVQSQRSCHEGYTLPLNGVSCPTVDYPCGKVPALERRGA 185  
183 SVAQATSSSGEAPDISITWKPYDAADLDPTENPFLLDNQTOPERGNLIRIVGGECK 242  
186 SNPGQ-----RIVGGKVP 199  
243 DECPQWQALLINEEGFCGGTILSEFYILTAHC---LYQAKRFKRVYGRNTEQEGG 299  
200 KGECPWQWQALLNGSTL-LCGSLLDTHWVWSAAHCFDKLSLRNLITVLGSHDLSHEGD 258  
300 EAVHEVEVVKINRFTKTYDFEDIAVLKTLPTITFRMNVAPACLPDRAEASTLMTQK 359  
259 EOVHRVAQLIMPDKVYVPGKTDHIALLRLLQPAALTNVNVPLCLPERNFSSTLITRFS 318

360 IVSGFGRTHREGROSTRKMLNLEVPVYDRNSCKLSS-----SFIITQNNMFCAGYDTKQDA 414  
319 RVSGWQQLLYRGALARELMAIDVPLMTQDCVQEQSEHNPSPGSPVETGNNMFCAGYLDGSKDA 378  
415 QDGGSGPHVTRFKDYFTVGTIVSGESCARGKGYTKYVTAFLKWLDRSMKTR 469  
379 CKGDSGGPHATSYHGTY-LTGVSWSGEGCARGVHGVYTRVSRDTEWLSRLMRSK 432

RESULT 11  
KF807  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999  
C:Accession: A31979; C20274  
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.  
J. Biol. Chem. 263, 14868-14877, 1988  
A:Title: Bovine factor VII: its purification and complete amino acid sequence.  
A:Reference number: A31979; MUID:89008362; PMID:3049594  
A:Accession: A31979  
A:Molecule type: protein  
A:Residues: 1-407 <TAK>  
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Accession: C20274  
A:Molecule type: protein  
A:Residues: 58-62, X' 64-68 <MCM>  
A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid  
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J. Biochem. 104, 867-868, 1988  
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood c  
A:Reference number: A44556; MUID:89213999; PMID:3149637  
A:Contents: annotation  
A:Note: structure and location of covalently bound carbohydrate  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the pr  
gulation factor IX in the presence of calcium and tissue factor  
A:Pathway: blood coagulation extrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu  
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MAL>  
F:1-44/Domain: Gla domain homology (fragment) <GLA>  
F:50-81/Domain: EGF homology <EG1>  
F:91-127/Domain: EGF homology <EG2>  
F:153-307/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F:153-307/Domain: trypsin homology <TRY>  
F:6, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35/Modified site: gamma-carboxyglutamic acid (Glu) #sta  
F:17-22, 50-61, 55-70, 72-81, 91-102, 98-112, 114-127, 135-262, 159-164, 178-194, 310-329, 340-3  
F:52/Binding site: carboxylate (Ser) (covalent) #status experimental  
F:63/Modified site: erythro-beta-hydroxyaspartic acid (asp) (partial) #status experim  
F:145, 203/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:152-153/Cleavage site: Arg-Ile (coagulation factor VIIa) #status experimental  
F:193, 242, 344/Active site: His, Asp, Ser #status predicted  
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 33.1%; Score 872; DB 1; Length 407;  
Best Local Similarity 38.7%; Pred. No. 2.7e-52;  
Matches 174; Conservative 71; Mismatches 137; Indels 68; Gaps 9;

41 ANSFLKEMKGLHLEKMEETCSYEAAREVFEDSKTNFENYKDKDQCTSPCQNGK 100  
1 ANSFLKEMKGLHLEKMEETCSYEAAREVFEDSKTNFENYKDKDQCTSPCQNGK 60  
101 CKDGLGEYTCCTLEGEGKNCEL--FTRKLCSLDNGDQDFCHEEQNS-VVCSARGYIL 157  
61 CEQRLSYICFCPDGPEGRNCTDKQSOLICANDNGCEQYCGADPGAGFCWCHEGYAL 120  
158 ADNGKACIPGPGK-QTLERRKSVAGATSSSGEAPDISITWKPYDAADLDPTENPF 216  
121 QADGVSCAPTVEYPCGKIPVLEKRNKSPGQ----- 151





A:Residues: 'D', 204, 'X', 206-211; 212, 'D', 214, 'X', 216-221, 'D' <AGA>  
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrazide  
 R:Di Scipio, R.G.; Kurachi, K.; Davie, E.W.  
 J. Clin. Invest. 61, 1528-1538, 1978  
 A:Title: Activation of human factor IX (Christmas factor).  
 A:Reference number: A18483; PMID:78194509; PMID:659613  
 A:Contents: annotation; activation; active site; carbohydrazide binding  
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.  
 Am. Soc. Genetol. Abstr. 64(Suppl.1), 262a, 1984  
 A:Reference number: A37569  
 A:Contents: annotation  
 A:Note: 194-Thr was also found  
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
 J. Biol. Chem. 259, 5698-5704, 1984  
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding  
 A:Reference number: A37543; PMID:84185715; PMID:6425296  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
 J. Biol. Chem. 260, 2583, 1985  
 A:Reference number: A37544  
 A:Contents: annotation; calcium binding, correction  
 R:Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
 Cell 45, 343-348, 1986  
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation  
 A:Reference number: A37545; PMID:86189947; PMID:3003023  
 A:Contents: annotation; signal sequence cleavage site  
 R:Suenhiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya, J.  
 J. Biol. Chem. 264, 21257-21265, 1989  
 A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan  
 A:Reference number: A30622; PMID:90078229; PMID:2592373  
 A:Contents: annotation; sequence of mutant B(M) Nagoya  
 A:Note: Carboxylation, glycosylation, and cleavage sites  
 R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee  
 submitted to the Brookhaven Protein Data Bank, November 1991  
 A:Reference number: A51252; PDB:1IXA  
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130  
 A:Note: recombinant form expressed in yeast  
 C:Comment: Factor IX is activated by factor Xla, which excises the activation peptide p  
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str  
 C:Genetics:  
 A:Gene: GPB-F9  
 A:Cross-references: GDB:119900; OMIM:306900  
 A:Map position: Xq27.1-Xq27.2  
 A:Intron: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
 A:Pathway: blood coagulation intrinsic pathway  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keyword: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglut  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-46/Domain: propeptide #status experimental <PPT>  
 F:31-91/Domain: Gla domain homology <Gla>  
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>  
 F:97-128/Domain: EGF homology <EGF>  
 F:134-170/Domain: EGF homology <EG>  
 F:192-226/Domain: activation peptide #status experimental <ACT>  
 F:227-456/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F:227-456/Domain: trypsin homology <TRY>  
 F:53-64, 61, 63, 66, 67, 73, 76, 77, 82, 86/Modified site: gamma-carboxyglutamic acid (Glu) #  
 F:64-69, 97-108, 102-117, 119-128, 134-145, 141-155, 157-170, 178-335, 352-268, 382-395, 407-435/  
 F:99/Binding site: carboxylate (Ser) (covalent) #status experimental  
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental  
 F:203, 213/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:205, 215/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental  
 Query Match 39.5%; Score 1041.5; DB 1; Length 461;  
 Best Local Similarity 44.8%; Pred. No. 8e-64;  
 Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;  
 9 LLSASLALLLGE-SLFIRQANNILARTRANS-FLEMKHGLERECMEETCSYEE 66

QY

Db 14 LITICLLGYLLSAECTVFLDHNANKILNRPKRYNSGKLEEFVQGNLRECEMEKSPFE 73  
 QY 67 AREVFEDSDKTFNFWNKYKDGOCETSPONQKCKDGLGEYTCCTCLEGFEGKNCBLFTR 126  
 Db 74 AREVFENTERTEFWKYVDGOCESNPLNGSGCKDDINSYECWCPFGFEGKNCBLDV- 132  
 QY 127 KLCSLDNGDCQFC-HEEQNSVVCSCARGVTLADNKGACITPTGYPGCKOTLERRRKRSVA 185  
 Db 133 -TCNINRGCEQFCCKNSADKNKVCSTEGYRLAENOKSCPEAVPFPGGRVSVQ----TS 187  
 QY 186 QATSSSGEAPDSITWPKPYDAADLDPTENPFDLLDFNOTQPERGNNLNRIVGGQCKDGE 245  
 Db 188 KLTRAFAVFPD-----VDVNSTEATILD-----NITQSTQSFNDFTRVVGGEADKPGQ 237  
 QY 246 CPQALLINEENGFCGGTILSEFYILTAHCLYQAKRKVRVGRDNTQEEGGEAVEHY 305  
 Db 238 FPMQVVL-NGKVDFAFCGGSIVNEKWLIVTAACHVETGVKTVVAGEHNIEETEHEQRNV 296  
 QY 306 EVVIKHNRFTK--ETVDFOIAVLRLKTPITFRNMNAPACILPERDMAESTLMTQKTGIVSG 363  
 Db 297 IRIIPHNNYNAINKYNHIDIALELDEPLVNSVYVTPICIADEYTNIFLKEGSGVSG 355  
 QY 364 FGRTHKGRQSTRLKMLEVYVDNRSKLSSTPITQNMFCAGYDPKQEDACQDGGSGPH 423  
 Db 356 WGRVFHKGKRSALVQLVPLVDRATCLRSTKFTIYNMFCAGFHGEGGRDSCQDGGSGPH 415  
 QY 424 VTRFKDTFYVTGTVSGSCARKGYIVTKYTAFLKWLIDRSMK 467  
 Db 416 VTEVGTSLTGTISMGECAMKGYITTKVSRVYVNWIKETK 459  
 RESULT 6  
 JQ0419  
 coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999  
 C:Accession: JQ0419; I49667  
 R:Wu, S.M.; Stafford, D.W.; Ware, J.  
 Gene 86, 275-278, 1990  
 A:Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.  
 A:Reference number: JQ0419; MUID:90215309; PMID:2323576  
 A:Accession: JQ0419  
 A:Molecule type: mRNA  
 A:Residues: 1-459 <WUS>  
 A:Cross-references: GB:M231109; NID:g193317; PIDN:AAA37629.1; PID:g387158  
 A:Experimental source: liver  
 R:Sarkar, G.; Koeberl, D.D.; Sommer, S.S.  
 Genomics 6, 133-143, 1990  
 A:Title: Direct sequencing of the activation peptide and the catalytic domain of the  
 A:Reference number: I49667  
 A:Accession: I49667  
 A:Status: preliminary; translated from GB/EMBL/DDBT  
 A:Molecule type: mRNA  
 A:Residues: 168-362, Q', 364-387, I', 389-451 <RES>  
 A:Cross-references: GB:M26236; NID:g193319; PIDN:AAA37630.1; PID:g193320  
 C:Comment: This protein plays a critical role in blood coagulation.  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu  
 F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:17-34/Domain: propeptide #status predicted <PRO>  
 F:19-79/Domain: Gla domain homology <Gla>  
 F:35-459/Product: coagulation factor IX #status predicted <MAT>  
 F:85-116/Domain: EGF homology <EG>  
 F:122-158/Domain: EGF homology <EG2>  
 F:225-452/Domain: trypsin homology <TRY>  
 F:41, 42, 49, 51, 54, 55, 60, 61, 64, 67, 70, 74/Modified site: gamma-carboxyglutamic acid (Glu)  
 F:52-57, 85-96, 90-105, 107-116, 122-133, 129-143, 145-158, 166-333, 250-266, 380-394, 405-433/  
 F:265, 313, 409/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 44.4%; Score 1039.5; DB 2; Length 459;

Matches 211; Conservative 78; Mismatches 151; Indels 35; Gaps 11;



C:Genetics:  
 A:Gene: F10  
 A:Map position: 13q34  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium ions  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GIA>  
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-233/Domain: activation peptide #status experimental <APT>  
 F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F:234-461/Domain: trypsin homology <TRY>  
 F:46-47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <SG>  
 F:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-341/Disulfide bonds: #status predicted <SIB>  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F:208, 485/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted  
 F:240-245, 260-276, 389-403, 414-442/Disulfide bonds: #status experimental  
 F:275, 321, 418/Active site: His, Asp, Ser #status predicted

Query Match 70.3%; Score 1851; DB 1; Length 492;

Best Local Similarity 69.8%; Pred. No. 4,1e-119;

Matches 340; Conservative 58; Mismatches 81; Indels 8; Gaps 4;

QY	5	LHLVLLSASLAGLLGSLFIRREQANNILARVTRANSFLEEMKKGHLERECMEETCSY	64
DB	5	LHLVLLSALGGLLRPAAGSVLPDRQHRVLRARRANSFLEEVKQGNLERECLEACSL	64
QY	65	EEAREVFSDSKTFEWNKFKDQCTSPQONOGCKDGLGEVTCCLGSEFGKNCLEF	124
DB	65	EEAREVFDAQDTDEFWSKYKDGQCGHPCNLGCHGDKGIGDYTCACGFEKNGCEFS	124
QY	125	TRKLCSDNGDCDFCHEEQNSVVCARGYTLADNGKACIPTGYPYCGKQTLERRKRSV	184
DB	125	TRKLCSDNGDCDFCHRESEVRSCAHGVLDGDSKSCVSTERFFCGNFTQGRSR--	182
QY	185	AQNTSSSGEAPDSITWPPYDAADLDPTENFDLLDFNQTQPERGD--NNITRVGGQECK	242
DB	183	-WAIHTSDALDASELHYDPADLSPTFESSLLDLGLNRTFESAGEDSGQVVRVIGGRDCA	241
QY	243	DGECPWQALLNEENEGFCGGTILSEFYILTAACHLYQAKRFVVRVGRNTEQEGEAV	302
DB	242	EGECPWQALLNEENEGFCGGTILSEFYILTAACHLYQAKRFVVRVGRNTEQEGEAV	301
QY	303	HEVEVYKHNFTKTYDFDIJAVLRKLTPTIFRNNVAPACLPEDMAESTIMTQKTGIS	362
DB	302	HEVEVYKHSRFVETDYDFDIJAVLRKLTPTIFRNNVAPACLPEDMAESTIMTQKTGIS	361
QY	363	FGFRTHEKRGROSTRKLMLEVPYVDRNSKLSLSSFIITQNMFCAGYDTKQEDACQDGGP	422
DB	362	FGFRTHEKGRSLSTKLMLEVPYVDRNSKLSLSSFIITQNMFCAGYDTKQEDACQDGGP	421
QY	423	HVTRFKDTYFTVGTIVSGEACARKGKGYITKVTAFKLRWIDRSMKTR--GLPKAKSH--AP	479
DB	422	HVTRFKDTYFTVGTIVSGEACARKGKGYITKVTAFKLRWIDRSMKTR--GLPKAKSH--AP	479
QY	480	EVITSSP	486
DB	482	ATWTVPP	488

RESULT 4

EXCH

coagulation factor Xa (EC 3.4.21.6) precursor - chicken

N:Alternate names: virus-activating proteinase

C:Species: Gallus gallus (chicken)  
 C:Date: 12-Feb-1993 #sequence:revision 07-Feb-1997 #text\_change 16-Jul-1999  
 C:Accession: S15838; S20380; S20381  
 R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; FEBS Lett. 283, 281-285, 1991  
 A:Title: Primary structure of the virus activating protease from chick embryo. Its id  
 A:Reference number: S15838; MUID:91257322; PMID:2044767  
 A:Accession: S15838  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-475 <SU>  
 A:Cross-references: DDBJ:D00844; NID:g222869; PIDN:BAA00724.1; PID:g222870  
 R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.  
 FEBS Lett. 296, 274-278, 1992  
 A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease respon  
 A:Reference number: S20380; MUID:92164779; PMID:1537403  
 A:Accession: S20380  
 A:Molecule type: protein  
 A:Residues: 41-55 <GO>  
 A:Accession: S20381  
 A:Molecule type: protein  
 A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium ions  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GIA>  
 F:41-185/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-167/Domain: EGF homology <EG2>  
 F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F:186-240/Domain: activation peptide #status predicted <APT>  
 F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F:241-168/Domain: trypsin homology <TRY>  
 F:46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu)  
 F:57-62, 90-101, 95-110, 112-121, 129-140, 136-152, 154-167, 175-348, 247-252, 267-283, 396-410  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:196, 207, 228, 285/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:282, 328, 425/Active site: His, Asp, Ser #status predicted

Query Match 54.1%; Score 1425; DB 1; Length 475;  
 Best Local Similarity 55.3%; Pred. No. 5,1e-90;  
 Matches 267; Conservative 71; Mismatches 123; Indels 22; Gaps 4;

QY	1	MGRPLHLVLLSASLAGLLGSLFIRREQANNILARVTRANSFLEEMKKGHLERECME	60
DB	1	MAGRLLLLLCALPDLELRAGGVFTKESADKFLERTRKANSFLEEMKQGNIERECNE	60
QY	61	TCSYEAREVFEVSDSKTFEWNKFKDQCTSPQONOGCKDGLGEVTCCLGSEFGKN	120
DB	61	RCSKEAREAFEDNEKTEEFWNYVDGQCSNPCHYGCGCKDGLGSLGTCSDGQGN	120
QY	121	CELFTKRLCSLNGDCDFC---HEEQNSVVCARGYTLADNGKACIPTGYPYCGKQTL	177
DB	121	CEFVTPKYCKINNGDCEQFCISKYSQKDVVSCSTSGVELAEDGKQCVSKVYPCGKVL	180
QY	178	ERRKRSVAQATSSSGEAPDSITWPPYDAADLDPT-----ENPFDLLDFNQTQPERGD	232
DB	181	KRIKRSVILPTNSNTATSD-----QDVSTNGSILEEFTTTTSTPPPPRNGSSI	232
QY	233	-----TRIVGGQECKDGECPWQALLNEENEGFCGGTILSEFYILTAACHLYQAKRFK	286
DB	233	TDPNVDTTRIVGGDECRPGCPWQAVLINEKEGFCGGTILNEDFILTAAHCINQSKIKV	292
QY	287	RVGDRNTEQEGEGEAVHEVEVYKHNFTKTYDFDIJAVLRKLTPTIFRNNVAPACLP	346
DB	293	VYGEVDREKEEHESETHTAEKIFVHSKYTAETVNDIALIKLKEPIQFSEYVVPACLPQA	352
QY	347	DWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSKLSLSSFIITQNMFCAG	406



A:Accession: I62745	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: DNA	
A:Residues: 295-383, G', 385-455 <MUR>	
A:Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396	
C:Function:	
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium	
A:Pathway: blood coagulation	
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology	
F:1-23/Domain: signal sequence #status predicted <SIG>	
F:24-40/Domain: propeptide #status predicted <PRO>	
F:25-84/Domain: Gla domain homology <GLA>	
F:41-179/Product: coagulation factor X light chain #status predicted <LCH>	
F:90-121/Domain: EGF homology <EGF>	
F:129-164/Domain: EGF homology <EG2>	
F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>	
F:183-231/Domain: activation peptide #status predicted <APT>	
F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>	
F:232-460/Domain: trypsin homology <TRY>	
F:46 47 54 56 59 60 65 66 69 72 79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <MOD>	
F:57-62 90-101 95-110 112-121 129-140 136-149 151-164 172-340 338-402 411-420/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted <MOD>	
F:187/Binding site: carboxylate (Asn) (covalent) #status experimental	
F:208/Binding site: carboxylate (Thr) (covalent) #status predicted	
F:218/Binding site: carboxylate (Asn) (covalent) #status predicted	
F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status predicted	
F:274,320,417/Active site: His, Asp, Ser #status predicted	
Query Match 74.3%; Score 1957; DB 1; Length 482;	
Best Local Similarity 74.2%; Pred. No. 2.3e-126;	
Matches 359; Conservative 54; Mismatches 163; Indels 8; Gaps 3;	
QY	1 MGRPLHLVLLSASLAGLLGSEFIRREOANNILARVTRANSFLERKMGHLERECME 60
DB	1 MESPVRLSLVYVLLASLLLPERSVFINRRANNVQLRRANSFFFEIKKGNLERECVE 60
QY	61 TCSYEAREVFEDSDKTNEFWNKYKDGQDETSPQNGKCKDGLGYETCTCLEGEGKN 120
DB	61 ICSPFEAREVFEDNEKTEFWNKYEDGQDESSPCNQNGECRDGLGYETCTCTEGEGKN 120
QY	121 CELFTRKCLSDNGDCDFCHEEONSVCSCARGYTLADNGKACIPGPPCKQTLERR 180
DB	121 CELFVRKCLSDNGDCDFCHEEONSVCSCARGYTLADNGKACIPGPPCKQTLERR 180
QY	181 KRSVAQATSSGEAPDSITWKPYDAADLPDENPDLDPENPDLDPENPDLDPENPDL 240
DB	181 KRSVALNTSSEPPEDLM---PDADILYTESPSELNKNKTEPEANSDDVIRIVGGQE 237
QY	241 CKDGCEPQWALLI-NEENEGFCGSTILSEFYLLTAACHLYQAKRFKRVGRVDRNTEQEEG 299
DB	238 CKRGCEPQWALLFSDDETDGFCGGTILNEFYLLTAACHLYQAKRFKRVGRVDRNTEQEEG 297
QY	300 EAVHEVEVVKHNFRTETVDFDIAVLRLKPTIFRNNVAPACLPEDWAEILMTQKGT 359
DB	298 EMVEHVDIMIKHNFRTETVDFDIAVLRLKPTIFRNNVAPACLPEDWAEILMTQKGT 357
QY	360 IVSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSSTFIQNMFCAGYDTPKQEDACOGDS 419
DB	358 IVSGFGRTHKGROSKVLMKMEVYVDRNCRSTFSIQNMFCAGYDTPKQEDACOGDS 417
QY	420 GGPHTVTRKDFYFTGVISWGESCARGKYGIYTKVTAFLKWDIRSMKTRGLPKAK---- 475
DB	418 GGPHTVTRKDFYFTGVISWGESCARGKYGIYTKVTAFLKWDIRSMKTRGLPKAK---- 475
QY	476 SHAP 479
DB	478 THPP 481

RESULT 3  
EXBO  
coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N:Alternate names: Stuart factor  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999  
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
R:Fung, M.R.; Campbell, R.W.; MacGillivray, T.A.  
Nucleic Acids Res. 12, 4481-4492, 1984  
A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing  
A:Reference number: A22867; MUID:84247315; PMID:6330671  
A:Accession: A22867  
A:Molecule type: mRNA  
A:Residues: 1-487 <FUNG>  
A:Cross-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193  
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
Biochemistry 19, 659-667, 1980  
A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
A:Reference number: A14997; MUID:80130563; PMID:6766735  
A:Accession: A14997  
A:Molecule type: protein  
A:Residues: 41-102, N', 104-180 <ENF>  
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Contents: annotation; revision to residue 103  
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
A:Reference number: A12030; MUID:76053069; PMID:1059093  
A:Accession: A12030  
A:Molecule type: protein  
A:Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492  
A:Note: carboxylate binding sites and disulfide bonds were determined  
R:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.  
J. Biol. Chem. 264, 16897-16904, 1989  
A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epiderm  
A:Reference number: A34412; MUID:89380326; PMID:2789221  
A:Accession: A34412  
A:Molecule type: protein  
A:Residues: 85-126 <PER>  
A:Note: beta-hydroxyaspartic acid site  
R:Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993  
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides  
A:Reference number: S39414; MUID:94062825; PMID:8243461  
A:Accession: S39414  
A:Molecule type: protein  
A:Residues: 183-196; 199-209; 216-233 <INO>  
A:Note: carboxylate binding sites  
R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
Biochemistry 11, 4899-4903, 1972  
A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mamm  
A:Reference number: A12453; MUID:73053314; PMID:4264286  
A:Contents: annotation; active site  
R:Fujikawa, K.; Titani, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha  
A:Reference number: A13504; MUID:76053121; PMID:1059122  
A:Contents: annotation; activation  
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
J. Biol. Chem. 259, 5705-5710, 1984  
A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxygluta  
A:Reference number: A38024; MUID:84185716; PMID:6546930  
A:Contents: annotation; calcium binding  
R:Morita, T.; Jackson, C.M.  
J. Biol. Chem. 261, 4008-4014, 1986  
A:Reference number: A38025; MUID:86140210; PMID:3949800  
A:Contents: annotation; sulfate binding  
C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
C:Comment: The two chains are formed from a single-chain precursor by the excision of  
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway)  
activation.  
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s  
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita



A:Accession: A21284  
A:Molecule type: mRNA  
A:Residues: 13-284, 'E', 289-488 <LE2>  
R:Cross-references: GB:K01886  
R:McMullen, B.A.; Fujikawa, K.; Kiesel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins  
Biochemistry 22, 2875-2884, 1983  
A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor  
A:Reference number: A20362; MUID:83257207; PMID:6871167  
A:Accession: A20362  
A:Molecule type: protein  
A:Residues: 41-179 <MCW>  
R:Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993  
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
A:Reference number: S39414; MUID:94062825; PMID:8243461  
A:Accession: S39415  
A:Molecule type: protein  
A:Residues: 183-234 <INO>  
A:Note: glycosylation sites  
A:Title: Identification and characterization of beta-hydroxyaspartic acid  
R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.  
Gene 84, 517-519, 1989  
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human  
A:Reference number: I54051; MUID:90128299; PMID:2612918  
A:Accession: I54051  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-23 <RES>  
A:Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330  
R:Padmanabhan, K.P.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla  
J. Mol. Biol. 232, 947-966, 1993  
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
A:Reference number: A49458; MUID:93360277; PMID:835279  
A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
C:Comment: The two chains held together by one disulfide bond are formed from a single-c  
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of  
C:Genetics:  
A:Gene: GDB:F10  
A:Cross-references: GDB:119890; OMTM:227600  
A:Map position: 13q34-13q34  
A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
A:Note: deficiency of this factor causes Stuart disease  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:41-179/Product: coagulation factor X light chain #status experimental <LCH>  
F:90-121/Domain: EGF homology <EG>  
F:123-164/Domain: EGF homology <EG2>  
F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
F:183-234/Domain: activation peptide #status experimental <APT>  
F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
F:235-462/Domain: trypsin homology <TRY>  
F:46.47.54.56.59.60.65.66.69.72.79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
F:57-62/Disulfide bonds: #status predicted  
F:90-101, 95-112, 112-121, 129-140, 136-149, 151-164, 172-342, 241-246, 261-277, 390-404, 415-443/  
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:199, 211/Binding site: carboxylate (Thr) (covalent) #status experimental  
F:221, 231/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
F:276, 322, 419/Active site: His, Asp, Ser #status experimental  
Query Match 99.8%; Score 2630; DB 1; Length 488;  
Best Local Similarity 99.8%; pred. No. 2.4e-172;  
Matches 487; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MGRPLHLVLSASLAGLLLGESLIRREQANNILAVTVTRANSFLEEMKKHGLERECMEE 60  
|||||  
DB 1 MGRPLHLVLSASLAGLLLGESLIRREQANNILAVTVTRANSFLEEMKKHGLERECMEE 60  
|||||

## RESULT 2

## EXRT

coagulation factor Xa (EC 3.4.21.6) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Jan-1995 #sequence\_revision 07-Feb-1997 #text\_change 08-Dec-2000

C:Accession: S49075; JC4670; PS0191; PS0190; I62745

R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.

Thromb. Res. 80, 63-73, 1995

A:Title: Evidence for competition between vitamin K-dependent clotting factors for in  
A:Reference number: A58498; MUID:96093366; PMID:8578539

A:Accession: S49075

A:Molecule type: mRNA

A:Residues: 1-482 &lt;STAL&gt;

A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601

A:Note: submitted to the EMBL Data Library, June 1994

A:Note: neither the complete nucleic acid sequence nor the complete translation are s  
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.

Gene 169, 269-273, 1996

A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.

A:Reference number: JC4670; MUID:96194815; PMID:8647460

A:Accession: JC4670

A:Molecule type: mRNA

A:Residues: 1-482 &lt;STAX&gt;

A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601

A:Experimental source: Cos-1 cell

R:Enjyoji, K.; Miyazaki, K.; Kato, H.

J. Biochem. 109, 890-898, 1991

A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat

A:Reference number: PS0190; MUID:92041742; PMID:1718949

A:Accession: PS0191

A:Molecule type: protein

A:Residues: 41-58, 'X', 60-65 &lt;ENJ1&gt;

A:Accession: PS0190

A:Molecule type: protein

A:Residues: 183-186, 'X', 188-207 &lt;ENJ2&gt;

R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.

Eur. J. Haematol. 52, 162-168, 1994

A:Title: Analysis of the partial nucleotide sequences and deduced primary structures

A:Reference number: I46196; MUID:94222160; PMID:8168596

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2003, 10:23:19 ; Search time 42 seconds

(without alignments)

1117.388 Million cell updates/sec

Title: US-09-632-722-2

Perfect score: 2634

Sequence: 1 MGRPLHLVLSASLACGLLL.....RGLPKAKSHAPEVITSSPLK 488

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database

PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2630	99.8	488	1 EXHU	coagulation factor
2	1957	74.3	482	1 EXRT	coagulation factor
3	1851	70.3	492	1 EXBO	coagulation factor
4	1425	54.1	475	1 EXCH	coagulation factor
5	1041.5	39.5	461	1 KFBU	coagulation factor
6	1039.5	39.5	459	2 JQ0419	coagulation factor
7	1032.5	39.2	452	1 A30351	coagulation factor
8	963	36.6	416	1 KFBO	coagulation factor
9	948	36.0	466	1 KFBU7	coagulation factor
10	945.5	35.9	443	2 I46932	coagulation factor
11	872	33.1	407	1 KFBO7	coagulation factor
12	872	33.1	456	1 KXBO	protein C (activat
13	861	32.7	461	1 S18994	protein C (activat
14	858	32.6	461	1 JX0210	protein C (activat
15	837	31.8	161	2 I62744	coagulation factor
16	827	31.4	461	1 KXHU	protein C (activat
17	766	29.1	161	2 I48158	coagulation factor
18	637	24.2	622	1 TBHU	thrombin (EC 3.4.2
19	621.5	23.6	618	2 A35827	thrombin (EC 3.4.2
20	598.5	22.7	625	1 TBBO	thrombin (EC 3.4.2
21	594.5	22.6	617	2 S10511	thrombin (EC 3.4.2
22	590.5	22.4	422	1 KXHUZ	plasma protein z p
23	568	21.6	275	2 I46712	factor IX - rabbit
24	566	21.5	282	2 I84621	coagulation factor
25	559.5	21.2	285	2 I48144	coagulation factor
26	544.5	20.7	271	2 I46580	factor IX - pig (f
27	521	19.8	274	2 I47078	coagulation factor
28	510	19.4	396	1 KXBOZ	plasma protein z -
29	435	16.5	235	2 E42696	thrombin (EC 3.4.2

## RESULT 1

EXHU

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N:Alternate names: Stuart factor

C:Species: Homo sapiens (man)

C:Date: 15-Nov-1984 #sequence revision 02-May-1994 #text\_change 08-Dec-2000

C:Accession: A24478; JQ0917; A2485; A25853; A22208; A21284; A20362; S39415; I54051;

R:Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.

Biochemistry 25, 5098-5102, 1986

A:Title: Gene for human Factor X: a blood coagulation factor whose gene organization

A:Reference number: A24478; MUID:87026600; PMID:3768336

A:Accession: A24478

A:Molecule type: DNA

A:Residues: 1-488 <LEY>

A:Cross-references: GB:L29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; PID:g182831

R:Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.

Gene 99, 291-294, 1991

A:Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human c

A:Reference number: JQ0917; MUID:91216473; PMID:1902434

A:Accession: JQ0917

A:Molecule type: mRNA

A:Residues: 1-488 <MES>

A:Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390

R:Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.

J. Biol. Chem. 267, 7395-7401, 1992

A:Title: Liver-specific expression of the gene coding for human factor X, a blood coa

A:Reference number: A2485; MUID:92218390; PMID:1313796

A:Accession: A2485

A:Molecule type: DNA

A:Residues: 1-15 <MIA>

A:Experimental source: liver

A:Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)

R:Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.

Gene 41, 311-314, 1986

A:Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A:Reference number: A25853; MUID:86221713; PMID:3011603

A:Accession: A25853

A:Molecule type: mRNA

A:Residues: 19-284, 'E', '289-488 <KAU>

A:Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336

R:Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A:Title: Characterization of an almost full-length cDNA coding for human blood coagul

A:Reference number: A22208; MUID:85216545; PMID:2582420

A:Accession: A22208

A:Molecule type: mRNA

A:Residues: 13-441, 'S', '443-488 <FUN>

A:Cross-references: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841

R:Leytus, S.P.; Chung, D.W.; Kiesel, W.; Kurachi, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A:Title: Characterization of a cDNA coding for human factor X.

A:Reference number: A21284; MUID:84222026; PMID:6587384

polyprotein - Afri  
plasma hyaluronan-  
t-plasminogen acti  
plasma hyaluronan-  
trypsin (EC 3.4.21  
t-plasminogen acti  
t-plasminogen acti  
trypsin (EC 3.4.21  
t-plasminogen acti  
thrombin (EC 3.4.2  
thrombin (EC 3.4.2  
Ra-reactive factor  
t-plasminogen acti  
u-plasminogen acti  
plasmin (EC 3.4.21  
thrombin (EC 3.4.2

30 429.5 16.3 1524 2 T30337  
31 423.5 16.1 560 1 JQ4795  
32 417 15.8 562 1 UKHUT  
33 416 15.8 558 2 JQ5878  
34 415.5 15.8 247 2 S05494  
35 415 15.8 559 1 A35029  
36 415 15.8 559 1 A29941  
37 412 15.6 247 2 A27547  
38 409.5 15.5 477 1 A34369  
39 406.5 15.4 234 2 F42696  
40 406 15.4 235 2 D42696  
41 404 15.3 686 1 A39271  
42 402.5 15.3 477 2 JS0598  
43 401.5 15.2 434 1 A35005  
44 398.5 15.1 455 2 A61545  
45 398 15.1 236 2 C42696

## ALIGNMENTS

288	HPNYKSTTDNDIALHQAATLSQTIYPICLPDGLAEARLNQAGQTT-LVTGWGTHS	346
369	EKGQSTR-----LKMLEVPPYDRNSCKLSSSFIITQNMFCAGYDTKQDACAQGSDDGPH	423
347	SREKEARNRRTFVLNFKIPVPHNECSEVMSNMVSENMLCAGILGDRQDACEGSDGGPM	406
424	VTREKDYFYVTGIVSNCECARGKGYITTKYTAFLKWIIDRSMKTRGLPKAKSHAP	479
407	VASPHGTWFLVLGVWSGEGCLLHNTGVYTKVSKRYLDWIHGHIROKEAPO-KSWAP	461

```

RESULT 15
US-10-182,263-3
; Sequence 3, Application US/10182263
; Publication No. US2003002354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182,263-3

```

Query Match	31.1%	Score 819;	DB 15;	Length 419;
Best Local Similarity	35.9%;	Prod. No. 1.3e-60;		
Matches	164;	Conservative 85;	Mismatches 152;	Indels 56; Gaps 8;
QY	41	ANSFLEEMKCHLERECMEETCSYEAREVFEFSDKTFNFWKYGDOGCE	TSP-----	94
Db	1	ANSFLEELRHGSLRECEIEICPEAKELFEDVDITLAFWSKHVDGQCLVLP	LEHPCA 60	
QY	95	--CQNGCKCKDGLGEYTCCTCLEGFEGKNCLELTKL--CSLDNGDCDQFCH	EEQNSVWC 151	
Db	61	SLCCGHGTCIDIGSFCDCRSQWGEGRFCQREVSFLCSLDGGCTHYCLE	EVGWRRCS 120	
QY	152	ARGVTLADNGKACIPTGYPGCK--OTLERKRSVAQATSSSGEAPDSIT	WKPYDAADL 209	
Db	121	APGYKLGDDLLQCHPAVKVFCGPRWKRMEKKRSHLAROTE-----	160	
QY	210	PTENPFDDLPNQTPERGDNNTIRIVGQECKDCGCPWQALLINEEGE	FCGGTILSEF 269	
Db	161	-----DQEQVFPRLTKGKTRRGDSPWQVLLDSKKKSACGAVLI	HPSS 204	
QY	270	YILTAACHLYQAKRFYRVGDRNTEQEGEAEVVEVVIKINRTFKTYD	FDIAVLRLK 329	
Db	205	WVLTAACHMDESKLLVRLGEYDLRWKQWELDLKEVFPHPNYSKST	TTONDLALHLA 264	
QY	330	TPITFRMNAACPLPERDMAESTL--MTQKTGIVSGFGRTHBKGRQ	STR-----LKMVE 382	
Db	265	QPATLSQITIVPICLPDSGLAERELNQAQET--LVTGWGYSHSREKA	RNRRTFVLNFIKI 323	
QY	383	PYVDRNSCKLSSFFITONMFCAGYDTKOEDACQDGGPHTRPKDFY	FVTGIVSWGES 442	
Db	374	PVPVPHNCSEVMNWSNMLCAGILGDRQDACEGSGPMVASPHGTW	FLVLGVLSWGE 383	
QY	443	CARKGKYGIYTKVTAFLKWDIRSMKTRGLPRAKSHAP	479	
Db	384	CGLLHNTGVYTKVSRYLDMTHGHIRDEKPAO--KSWAP	419	

Query Match		32.4%; Score 852.5; DB 16; Length 406;
Best Local Similarity		36.9%; Pred. No. 1.9e-63;
Matches		167; Conservative 76; Mismatches 147; Indels 63; Gaps 8;
QY	41	ANSFLEEMKKHGLERECMEETCSYEAREVFEDSDKTNEFWNKYKDGOCETSPOCQOK 100
DB	1	ANAFLLXLRPSGLXRXKXQCXFXKXKXIFKDXATKLFWSISYDQGCASSPCQNGS 60
QY	101	CKDGLGEYCTCLGEGEGNCELFTPK-----LCSLDNGCDQFCHEEQNSV-VCSARGY 155
DB	61	CKDQLSYICFCLPAPEGRNCE--THKDQLICVNEGGEQYCSDHGTGKRSCHHEGY 118
QY	156	TLADNCKACIPTGYPCKG-QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENP 214
DB	119	SLADGVSCTPVEYFCGPILEKXNASKPOG----- 151
QY	215	FLLDLDNQTQPERGDNLLTRIVGGQCKDGECPQWALLNENEGFCGGTILSEYILTA 274
DB	152	-----RIVGGKVCPRKGECPWQVLL-VNGAQLCGGTLLNTIWWVSA 191
QY	275	AHCLYOAKRFK---VRVGDNTTQEEGGEAVHEVEVVIKHNRTKETYDFDIIVLRLKTP 331
DB	192	AHCFDKIKWNRNLIIVGHEHJSEHGDGQSRRAQVIIPSTVPGTTHDIALRLKHP 251
QY	332	ITFRMNVAPACLPEDWAESTLMTQKTGIVSGFGRTHKRGOSTRLKMLEVPYVDRNSC- 390
DB	252	VLTLDHVPCLPRTFSELTAFVRFSLVSGWQLLDRGATALEMLVNLVPRMTQDCL 311
QY	391	-----KLSSPFIITONMFCAGYTKQEDACQSGGPHVTRFKDTYFVTGIVSWGESCARK 446
DB	312	QOSKRVGDSNITEYMFACYSGDSKDSKSGSGPHATHYRTGTYLTGIVSWGQCATV 371
QY	447	GKGYITKTAFLKWDIRSMKTRGLPKAKSHAP 479
DB	372	GHEGVYTRVSOYIEWLQKLMRSEPRPGVILLRAP 404
RESULT 13		
US-09-978-917A-2		
; Sequence 2, Application US/09978917A		
; Publication No. US20030027299A1		
; GENERAL INFORMATION:		
; APPLICANT: Maxygen Aps; Maxygen Holdings		
; TITLE OF INVENTION: Protein C or activated protein C-like molecules		
; FILE REFERENCE: 0219us310 - protein C		
; CURRENT APPLICATION NUMBER: US/09/978,917A		
; CURRENT FILING DATE: 2001-10-17		
; NUMBER OF SEQ ID NOS: 48		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 2		
; LENGTH: 461		
; TYPE: PRT		
; ORGANISM: Homo sapiens		
; FEATURE:		
; NAME/KEY: SIGNAL		
; LOCATION: (1)...(42)		
; FEATURE:		
; NAME/KEY: CHAIN		
; LOCATION: (43)...(461)		
US-09-978-917A-2		
Query Match		31.4%; Score 827; DB 11; Length 461;
Best Local Similarity		35.3%; Pred. No. 3.1e-61;
Matches		168; Conservative 92; Mismatches 160; Indels 56; Gaps 9;
QY	22	ESLFIREFQANNILARVTRANSFLEEMKKHGLERECMEETCSYEAREVFEDSDKTNEFW 81
DB	24	DSVFSSSERAHQVLRIRKRANSFLEELRHSSLERECIEICDFEAEKEIFQNVDDTLAFW 83
QY	82	NKYKDGQOCETSP-----CONQCKKDGIGETCTCLEGFEKNCLELFTKRL-CSLD 132
DB	84	SKHVDGQCLVLPLEHPCASLCCHGTCTIDGIFSFCDCRSRSGWGRFCQREVSFLNCSLD 143
QY	133	NGDCDOFCHEEQNSVVCSCARGYTLADNCKACIPTGYPCKGK--OTLERRKRSVAQATSS 190
DB	144	NGGTHYCLEEVGWRRCSCAPGYKLGDDLLQCHPAVKFPCGPRWKRMEKRRSHLKRDTED 203
QY	191	SGEAPDSITWKPYDAADLDPTENPFDLLDFNQTOPERGDNNLTRIVGGQCKDGECPWQA 250
DB	204	QED-----QVDP-----RLIDGKMTFRGDSPPQV 227
QY	251	LLINEENEGFCGGTILSEYILTAHCLYOAKRFKRVGVDRNTEQEEGGEAVHEVEVVIK 310
DB	228	VLLDSKKKLACGAVLIHPSWLTAACHMDESKLLVRLGEYDLRRWEKWLDDIKEVEFV 287
RESULT 14		
US-10-182-263-2		
; Sequence 2, Application US/10182263		
; Publication No. US20030022354A1		
; GENERAL INFORMATION:		
; APPLICANT: Jones, Bryan E		
; APPLICANT: Grinnell, Brian W		
; TITLE OF INVENTION: PROTEIN C DERIVATIVES		
; FILE REFERENCE: X-13611		
; CURRENT APPLICATION NUMBER: US/10/182,263		
; CURRENT FILING DATE: 2002-07-22		
; PRIOR APPLICATION NUMBER: 60/181948		
; PRIOR FILING DATE: 2002-02-11		
; PRIOR APPLICATION NUMBER: 60/189199		
; PRIOR FILING DATE: 2000-03-14		
; NUMBER OF SEQ ID NOS: 12		
; SOFTWARE: PatentIn version 3.1		
; SEQ ID NO 2		
; LENGTH: 461		
; TYPE: PRT		
; ORGANISM: Homo sapiens		
US-10-182-263-2		
Query Match		31.4%; Score 827; DB 15; Length 461;
Best Local Similarity		35.3%; Pred. No. 3.1e-61;
Matches		168; Conservative 92; Mismatches 160; Indels 56; Gaps 9;
QY	22	ESLFIREFQANNILARVTRANSFLEEMKKHGLERECMEETCSYEAREVFEDSDKTNEFW 81
DB	24	DSVFSSSERAHQVLRIRKRANSFLEELRHSSLERECIEICDFEAEKEIFQNVDDTLAFW 83
QY	82	NKYKDGQOCETSP-----CONQCKKDGIGETCTCLEGFEKNCLELFTKRL-CSLD 132
DB	84	SKHVDGQCLVLPLEHPCASLCCHGTCTIDGIFSFCDCRSRSGWGRFCQREVSFLNCSLD 143
QY	133	NGDCDOFCHEEQNSVVCSCARGYTLADNCKACIPTGYPCKGK--OTLERRKRSVAQATSS 190
DB	144	NGGTHYCLEEVGWRRCSCAPGYKLGDDLLQCHPAVKFPCGPRWKRMEKRRSHLKRDTED 203
QY	191	SGEAPDSITWKPYDAADLDPTENPFDLLDFNQTOPERGDNNLTRIVGGQCKDGECPWQA 250
DB	204	QED-----QVDP-----RLIDGKMTFRGDSPPQV 227
QY	251	LLINEENEGFCGGTILSEYILTAHCLYOAKRFKRVGVDRNTEQEEGGEAVHEVEVVIK 310
DB	228	VLLDSKKKLACGAVLIHPSWLTAACHMDESKLLVRLGEYDLRRWEKWLDDIKEVEFV 287

```
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-10-109 498-1

Query Match      32.4%; Score 852.5; DB 15; Length 406;
Best Local Similarity 36.9%; Pred. No. 1.9e-63;
Matches 167; Conservative 76; Mismatches 147; Indels 63; Gaps 8;

41  ANSFLEEMKKGHLERECMEETCSYEAREVEFSDKTNFENWNYKDGDCQETSPCQNGK 100
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1  ANAFLXLRPGSLRXKXKXQCSFXARXIFKDAKXKLFWISYSDGDCASSPCQNGGS 60
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
101 CKDGLGEYTCLEGFEGKNCLELFRK---LCSLDNGDCDFCHEEONS-VCSARGY 155
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
61 CKDQLQSYICFCLPAFEGNCE--THKDDQLICVNEGCGEQYCSDHGTGKRSRCRCHGY 118
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
156 TLADNGKACIPTGYPGCK-QTLERRKRSVAQATSSSGEAPDSITWKPYPDAADLDPTNP 214
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
119 SLLADGVSCPTVEYPCGKIPILEKRNASKPQG----- 151
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
215 FDLLEDNQTQPERGDNNTLRIVGGQCKDGECPQWQALLINEENGFCGGTILSEFYILTA 274
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
152 -----RIVGKVCYKPCGEPQWVLL--VNGAQLCGGTINTIWWVSA 191
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
275 AHCLYQAKRFK---VRVGRNTEQEGGEAVHEVEVVIKHNRTKETYDFDIIVLRKTP 331
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
192 AHCFDKIKNRNLIAVLGEHDLSEHDGEQSRVAQVIIPSTVPGTTNHDIALRLHQP 251
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
332 ITRFMNAPACLPEDRWAEETLMTQKTVGSGFRTHKGRQSTRLKMLEVYPYVDNRSC- 390
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
252 VVLTDHVVPLCLPTEFSERTLAFVRSLSVSGWQLLDRGATALELVNVPRLMTQDCL 311
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
391 ----KLSSSFIITQNMFCAGYDTKQEDACQDGGPHVTRFKDTEYFTVGVSWGESCAR 446
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
312 QOSRKVGDSNPITETMFCAGYSDGSKDCKSGDGGPHATHYRGTYLTGTIVSGGCGCATV 371
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
447 GKYGIYTKVTAFLKWDIRSMKTRGLPKAKSHAP 479
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
372 GHFGYTRVSYQIEWLQKLMRSEPRPGVLLRAP 404
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 11
US-10-255-032-1
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
```

```
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-255-032-1

Query Match      32.4%; Score 852.5; DB 15; Length 406;
Best Local Similarity 36.9%; Pred. No. 1.9e-63;
Matches 167; Conservative 76; Mismatches 147; Indels 63; Gaps 8;

41  ANSFLEEMKKGHLERECMEETCSYEAREVEFSDKTNFENWNYKDGDCQETSPCQNGK 100
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1  ANAFLXLRPGSLRXKXKXQCSFXARXIFKDAKXKLFWISYSDGDCASSPCQNGGS 60
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
101 CKDGLGEYTCLEGFEGKNCLELFRK---LCSLDNGDCDFCHEEONS-VCSARGY 155
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
61 CKDQLQSYICFCLPAFEGNCE--THKDDQLICVNEGCGEQYCSDHGTGKRSRCRCHGY 118
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
156 TLADNGKACIPTGYPGCK-QTLERRKRSVAQATSSSGEAPDSITWKPYPDAADLDPTNP 214
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
119 SLLADGVSCPTVEYPCGKIPILEKRNASKPQG----- 151
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
215 FDLLEDNQTQPERGDNNTLRIVGGQCKDGECPQWQALLINEENGFCGGTILSEFYILTA 274
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
152 -----RIVGKVCYKPCGEPQWVLL--VNGAQLCGGTINTIWWVSA 191
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
275 AHCLYQAKRFK---VRVGRNTEQEGGEAVHEVEVVIKHNRTKETYDFDIIVLRKTP 331
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
192 AHCFDKIKNRNLIAVLGEHDLSEHDGEQSRVAQVIIPSTVPGTTNHDIALRLHQP 251
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
332 ITRFMNAPACLPEDRWAEETLMTQKTVGSGFRTHKGRQSTRLKMLEVYPYVDNRSC- 390
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
252 VVLTDHVVPLCLPTEFSERTLAFVRSLSVSGWQLLDRGATALELVNVPRLMTQDCL 311
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
391 ----KLSSSFIITQNMFCAGYDTKQEDACQDGGPHVTRFKDTEYFTVGVSWGESCAR 446
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
312 QOSRKVGDSNPITETMFCAGYSDGSKDCKSGDGGPHATHYRGTYLTGTIVSGGCGCATV 371
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
447 GKYGIYTKVTAFLKWDIRSMKTRGLPKAKSHAP 479
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
372 GHFGYTRVSYQIEWLQKLMRSEPRPGVLLRAP 404
    ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 12
US-10-281-727-1
; Sequence 1, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PA 2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1
```

APPLICANT: BORNAES, CLAUS  
TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES  
FILE REFERENCE: 31-001100US  
CURRENT APPLICATION NUMBER: US/09/782,587B  
CURRENT FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: PA 2000 00218  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: 60/184,036  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: 60/241,916  
PRIOR FILING DATE: 2000-10-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3

LENGTH: 406

TYPE: PRT

ORGANISM: Homo sapiens

US-09-782,587B-3

Query Match 34.5%; Score 909.5; DB 11; Length 406;

Best Local Similarity 38.9%; Pred. No. 3.1e-68;

Matches 176; Conservative 77; Mismatches 137; Indels 63; Gaps 8;

Qy 41 ANSFLEEMKKGHLERECMETCSYEAREVFEDSDTNEFWNKYKDGQOCETSPCONQK 100

Db 1 ANAFLELRPGSLERECQCSFEAREIFKDAERTKLFWISYSDGQOCASSPCQNGS 60

Qy 101 CKDGLGYTCTCLEGPEGKNCLEFTRK----LCSLDNGDCDQFCHEEQNSV-VCSCARG 155

Db 61 CKDQLQSYICFCLPAFEGNCE--THKDDQLICVNGGCEQYCSHTGTKRSCRCHEG 118

Qy 156 TLADNGKACIPTGYPGCK-QTLERKRKRSVAQATSSSGEAPDSITWKPYDAADLDPTNP 214

Db 119 SLLADGVSCPTVEYPCGKIPILEKRNASKPQG----- 151

Qy 215 FDLDFNQTPERGDNLLTRIVGQECDCGCPQWALLINEEGFCGGTILSEFVILTA 274

Db 152 -----RIVGGKVCPCGECPCWQVLLL-VNGAQLCGGTLLNTIWVSA 191

Qy 275 AHCLYQAKRFK---VRVGDNRNTEQEGGEAVHEVVEVVKHNRTTKETDFDIARLTKP 331

Db 192 AHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRAQVVIIPSTVPGTTNHDIALRLHQP 251

Qy 332 ITRFMNVPACLPERDWAESTLMTQKTGIVSGFGRTHEKGQSTRKLMLEVPYVDNRSC- 390

Db 252 VVLTDRHVPLCLPRTESRTLAFVRSLSVSGWQLDRGATALEMLVNLVPRMTQDCL 311

Qy 391 ----KLSSSFIITONMFCAGYDTKQEDACQDGGGPHVTRFKDTYFVTGIVSWGESCARK 446

Db 312 QQSRKVGDSFNITEYMFACYSKGDSCKGSGGPHATHYRGTWLTGIVSWGQCATV 371

Qy 447 GKGIVTKYTAFLKWIIDRSMTKRGPLKAKSHAP 479

Db 372 GHFGVTVRSQYIEWLQKLMRSEPRPGVLLRAP 404

RESULT 9

US-09-782,587B-1

Sequence 1, Application US/09782587B

Publication No. US20030096338A1

GENERAL INFORMATION:

APPLICANT: PEDERSEN, ANDERS H.

APPLICANT: ANDERSON, KIM V.

APPLICANT: BORNAES, CLAUS

TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES

FILE REFERENCE: 31-001100US

CURRENT APPLICATION NUMBER: US/09/782,587B

CURRENT FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: PA 2000 00218

PRIOR FILING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: 60/184,036

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 60/241,916

PRIOR FILING DATE: 2000-10-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 406

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD\_RES

LOCATION: (6)..(7)

OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

NAME/KEY: MOD\_RES

LOCATION: (14)

OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

NAME/KEY: MOD\_RES

LOCATION: (16)

OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

NAME/KEY: MOD\_RES

LOCATION: (19)..(20)

OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

NAME/KEY: MOD\_RES

LOCATION: (25)..(26)

OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

NAME/KEY: MOD\_RES

LOCATION: (29)

OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

NAME/KEY: MOD\_RES

LOCATION: (35)

OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

US-09-782-587B-1

Query Match

Best Local Similarity

Matches 167; Conservative

76; Mismatches 147; Indels 63; Gaps 8;

Qy 41 ANSFLEEMKKGHLERECMETCSYEAREVFEDSDTNEFWNKYKDGQOCETSPCONQK 100

Db 1 ANAFLELRPGSLRXCKXXQCXXARXIFKDAERTKLFWISYSDGQOCASSPCQNGS 60

Qy 101 CKDGLGYTCTCLEGPEGKNCLEFTRK----LCSLDNGDCDQFCHEEQNSV-VCSCARG 155

Db 61 CKDQLQSYICFCLPAFEGNCE--THKDDQLICVNGGCEQYCSHTGTKRSCRCHEG 118

Qy 156 TLADNGKACIPTGYPGCK-QTLERKRKRSVAQATSSSGEAPDSITWKPYDAADLDPTNP 214

Db 119 SLLADGVSCPTVEYPCGKIPILEKRNASKPQG----- 151

Qy 215 FDLDFNQTPERGDNLLTRIVGQECDCGCPQWALLINEEGFCGGTILSEFVILTA 274

Db 152 -----RIVGGKVCPCGECPCWQVLLL-VNGAQLCGGTLLNTIWVSA 191

Qy 275 AHCLYQAKRFK---VRVGDNRNTEQEGGEAVHEVVEVVKHNRTTKETDFDIARLTKP 331

Db 192 AHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRAQVVIIPSTVPGTTNHDIALRLHQP 251

Qy 332 ITRFMNVPACLPERDWAESTLMTQKTGIVSGFGRTHEKGQSTRKLMLEVPYVDNRSC- 390

Db 252 VVLTDRHVPLCLPRTESRTLAFVRSLSVSGWQLDRGATALEMLVNLVPRMTQDCL 311

Qy 391 ----KLSSSFIITONMFCAGYDTKQEDACQDGGGPHVTRFKDTYFVTGIVSWGESCARK 446

Db 312 QQSRKVGDSFNITEYMFACYSKGDSCKGSGGPHATHYRGTWLTGIVSWGQCATV 371

Qy 447 GKGIVTKYTAFLKWIIDRSMTKRGPLKAKSHAP 479

Db 372 GHFGVTVRSQYIEWLQKLMRSEPRPGVLLRAP 404

RESULT 10

US-10-109-498-1

Sequence 1, Application US/10109498

Publication No. US20030044908A1

GENERAL INFORMATION:

Db 188 KLTRATVFPD-----VDYVNSTEAETILD-----NITQSTQSFNDFTRVVGDEDAKPGQ 237  
QY 246 CPWQALLNEEGFCGTTILSEFYILTAACHLYQAKREKVRVGDNRNTEQEGGEAVHEV 305  
Db 238 FPMQVVL-NGKVDACGSGIVNEKWIYTAACHVETGKITYVAGEHNTEETHEHQKRV 296  
QY 306 EVVVKHNRFTK--EYDFEDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKTIVSG 363  
Db 297 IRIIPHHYNAANKYNHDIALLLEDEPLVNSVYTPICIAKVEY-NIFLKFGSGYVG 355  
QY 364 FORTHEKROSTRKMLKLEVPVVDNRNSKLSSTFIITQNMFCAGYDTQEDACQDSCGGPH 423  
Db 356 MGRVHKRSALVQLYLRVPLVDRATLURSTKFTIYNMFCAGFHEGGRDSCQDSCGGPH 415  
QY 424 VTRFDYFTVIGVSWGSCARKGKIYITVKTATFLKWDIDRSMK 467  
Db 416 VTEVGTGSLTGLIISWGECAKMGKIYITVKSRYVNVKIKETK 459

RESULT 6  
US-09-118 748-2  
; Sequence 2, Application US/09118748A  
; Patent No. US20020031799A1  
; GENERAL INFORMATION:  
; APPLICANT: Stafford, Darrel W.  
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 5470-183  
; CURRENT APPLICATION NUMBER: US/09/118,748A  
; EARLIER FILING DATE: 1998-07-17  
; EARLIER APPLICATION NUMBER: 60/053,571  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-118 748-2

Query Match 37.8%; Score 996.5; DB 9; Length 415;  
Best Local Similarity 45.1%; Pred. No. 1.6e-75;  
Matches 192; Conservative 71; Mismatches 142; Indels 21; Gaps 8;

QY 45 LEEMKKHLEECMEETCSVEAREVEFSDSKTNEFWNKYKDGQCEPSCQNGKCKDG 104  
Db 6 LEFVQGNLERECMEKCSFEAREVEFENTERTEFWKQYVGDQCESNPLNGGCKDD 65  
QY 105 LGEVTCCTLEGFEKNCLELTKRLCSLDNGDCDQFC-HEQNSVVCSCARGYTLADNGKA 163  
Db 66 INSTECWCPGFEKNCLELDV--TCNKNKRCQFCQKNSADNKKVVCSTEGYRLAENQKS 123  
QY 164 CIPGPGKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPDLDPNOT 223  
Db 124 CEPAPVPCGVRVSQ----TSKLTRETFPD-----VDYVNSTEAETILD-----NIT 169  
QY 224 QPERGNNLRIVGCGQCKGECQWQALLNEENEGFCGTTILSEFYILTAACHLYQAKR 283  
Db 170 QSTQSFNDFTRVVGDEDAKPGQVQVVL-NGKVDACGSGIVNEKWIYTAACHVETGK 228  
QY 284 FKVRVGDNRNTEQEGGEAVHEVVIKHNRFK--EYDFEDIAVLRLKTPITFRMNVAPA 341  
Db 229 ITVVAGEHNTEETHEQKRVIRIIPHHYNAANKYNHDIALLLEDEPLVNSVYTP 288  
QY 342 CLPERDWAESTLMTQKTIVSGFGRTHKGRQSTRKMLKLEVPVVDNRNSKLSSTFIITON 401  
Db 289 CIADKEVT-NIFLKFGSGYVSGWRVPHKGRSALVQLYLRVPLVDRATCLASTKFTIYN 347  
QY 402 MFCAGYDTQEDACQDSCGGPHTRFKDTYFTVIGVSWGSCARKGKIYITVKTATFLK 461  
Db 348 MFCAGFHEGGRDSCQDSCGGPHVTEVGTSLTGLIISWGECAKMGKIYITVKSRYVNV 407

QY 462 IDRSMK 467  
Db 408 IKEKTK 413

RESULT 7  
US-10-017-122-2  
; Sequence 2, Application US/10017122  
; Publication No. US20030087244A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Jeanette  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE  
; FILE REFERENCE: MMI-007  
; CURRENT APPLICATION NUMBER: US/10/017,122  
; CURRENT FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: 60/327,487  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-122-2

Query Match 36.0%; Score 948; DB 15; Length 466;  
Best Local Similarity 36.9%; Pred. No. 2.2e-71;  
Matches 189; Conservative 86; Mismatches 155; Indels 82; Gaps 9;

QY 1 MGRPLHLVLSASLAGLLLLG-----ESLFTIRREQANNILARVTRA 41  
Db 2 VSOALRLCLLLGLQGLAAGVAKASGETRDMPKPGPHRVFVTQEEAHGVLHRRRA 61  
QY 42 NSPLEEMKKHLEECMEETCSVEAREVEFSDSKTNEFWNKYKDGQCEPSCQNGKCK 101  
Db 62 NAFLEELRPGSLERECEKQCSFEAREIFKDAERTKLFWISYDGDQACASPCQNGSC 121  
QY 102 KDGLGTYCTCLEGFEKNCLELTKR-----LCSLNGDCDQFCHEEQNSV-VCSARGYT 156  
Db 122 KDQLQSYICFCPLPAFGRNCE--THKDDQLICVNGGCEQYCSDHGTGKRSRCHEGYS 179  
QY 157 LADNGKACIPTGYPGCK-OTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENP 215  
Db 180 LADGVCSTPTVEYPCGKIPILEKRNASKPQ----- 211  
QY 216 DILLDFNQTQPERGNNLRIVGQCKGECQWQALLNEENEGFCGTTILSEFYILTA 275  
Db 212 -----RIVGKVCYKPCGECQWQVLLL-VNGAQLCGGTLLIITVWVSA 252  
QY 276 HCLYQAKRPF---VRVGDNRNTEQEGGEAVHEVVIKHNRFKTYDFDIAVLRLKTP 332  
Db 253 HCFDKIKNWRNLIAVLGEHDLSEHDDEQSRRAQVITPSTVYVPGTTHDIALRLHQP 312  
QY 333 TFRMNVAPACLPERDWAESTLMTQKTIVSGFGRTHKGRQSTRKMLKLEVPVVDNRNSC 390  
Db 313 VITDHHVPLCLPERTFSERTLAFVRFSLVSGWGLDGRGATALEMLVNLVPLMTQDC 372  
QY 391 ---KLSSFTIITQNMFCAGYDTQEDACQDSCGGPHTRFKDTYFTVIGVSWGSCARKG 447  
Db 373 QSRKVCDSNITEYMEFCAGYSQSKDCKGDSGSGPHATHYRGTWTWLTGIVSGGCATVG 432  
QY 448 KYGIYTKVTAFLKWDIDRSMKTRGLPKAKSHAP 479  
Db 433 HFGVTVRSQYIEWLQKLMSRSEPRPGVLLRAP 464

RESULT 8  
US-09-782-587B-3  
; Sequence 3, Application US/09782587B  
; Publication No. US20030096338A1  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, ANDERS H.  
; APPLICANT: ANDERSON, KIM V.

Query Match 39.5%; Score 1041.5; DB 15; Length 461;  
Best Local Similarity 44.8%; Pred. No. 3e-79;  
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

QY 9 LLSASLAGLLGGE-SLFIRREOANNILARVTRANS-FLEEMKKGHLERECMEETSCEE 66  
DB 14 LITICLLGYLLSAECTVFLDHENANKILNRPKNYSKLEEFVQGNLERECMEEKCSFEE 73  
QY 67 AREVFEDSDKTNEFWNKYKDGOCETSPQONQCKDKGLGEYCTCTCLEGFEKGNCELFTFR 126  
DB 74 AREVFENTERTEFWKQYVDGQCESNCLNGSGCKDDINSYECWCPFGFEKGNCELVD- 132  
QY 127 KLCSLDNGDCQDFC-HEEQNSVVCSCARGYTLDNGKACIPTGYPGCGKOTLERKRSVA 185  
DB 133 -TCNKNRGCEQFCCKNSADNKVVCSTEGYRLAENQKSCPEAVPPFCGRVSVSQ---TS 187  
QY 186 QATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNLTRIVGGQCKDGE 245  
DB 188 KLTRAEAVFPD-----VDYVNSTEAETILD---NITQSTQSFNDFTRVVGEDAKPGQ 237  
QY 246 CPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKVRVGRDNTQEEGGEAVHEV 305  
DB 238 FPMQVVL-NGKVDACGGSIVNEKWIIVTAACHVETGVKITVVAAGEHNIEETEHEKRN 296  
QY 306 EVVIKHNRFK--ETYDFDIAVLRLKTPITFRMNVAPACIPERDWAESTIMTQKTGIVSG 363  
DB 297 IRIIPHHYNAINKYNHDIALLDELPLVNSVYTPICIAKEYT-NIFLKFSGYVSS 355  
QY 364 FGRTHKGRSTRKMLVYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGSGPH 423  
DB 356 WGRVFKHGRSALVQLVLRVPLVDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQDGGSGPH 415  
QY 424 VTRFKDITYFTVGTIVSWGESCARCKGYIKYTKVAFKLKWDIRSMK 467  
DB 416 VTEVEGTSFLTGLIISWGECEAMKGYIKYTKVSRVYNNIKETK 459

RESULT 4  
US-10-132-829-5  
; Sequence 5, Application US/10132829  
; Publication No. US20030044982A1  
; GENERAL INFORMATION:  
; APPLICANT: Chien, Kenneth R  
; APPLICANT: Hoshijima, Masahiko  
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII  
; TITLE OF INVENTION: with vesicle vector  
; FILE REFERENCE: 6627-PAL170  
; CURRENT APPLICATION NUMBER: US/10132,829  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: 60/286,314  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-132-829-5

Query Match 39.58; Score 1039.5; DB 15; Length 461;  
Best Local Similarity 44.8%; Pred. No. 4.4e-79;  
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

QY 9 LLSASLAGLLGGE-SLFIRREOANNILARVTRANS-FLEEMKKGHLERECMEETSCEE 66  
DB 14 LITICLLGYLLSAECTVFLDHENANKILNRPKNYSKLEEFVQGNLERECMEEKCSFEE 73  
QY 67 AREVFEDSDKTNEFWNKYKDGOCETSPQONQCKDKGLGEYCTCTCLEGFEKGNCELFTFR 126  
DB 74 AREVFENTERTEFWKQYVDGQCESNCLNGSGCKDDINSYECWCPFGFEKGNCELVD- 132  
QY 127 KLCSLDNGDCQDFC-HEEQNSVVCSCARGYTLDNGKACIPTGYPGCGKOTLERKRSVA 185

QY 133 -TCNKNRGCEQFCCKNSADNKVVCSTEGYRLAENQKSCPEAVPPFCGRVSVSQ---TS 187  
QY 186 QATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNLTRIVGGQCKDGE 245  
DB 188 KLTRAEAVFPD-----VDYVNSTEAETILD---NITQSTQSFNDFTRVVGEDAKPGQ 237  
QY 246 CPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKVRVGRDNTQEEGGEAVHEV 305  
DB 238 FPMQVVL-NGKVDACGGSIVNEKWIIVTAACHVETGVKITVVAAGEHNIEETEHEKRN 296  
QY 306 EVVIKHNRFK--ETYDFDIAVLRLKTPITFRMNVAPACIPERDWAESTIMTQKTGIVSG 363  
DB 297 IRIIPHHYNAINKYNHDIALLDELPLVNSVYTPICIAKEYT-NIFLKFSGYVSS 355  
QY 364 FGRTHKGRSTRKMLVYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGSGPH 423  
DB 356 WGRVFKHGRSALVQLVLRVPLVDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQDGGSGPH 415  
QY 424 VTRFKDITYFTVGTIVSWGESCARCKGYIKYTKVAFKLKWDIRSMK 467  
DB 416 VTEVEGTSFLTGLIISWGECEAMKGYIKYTKVSRVYNNIKETK 459

RESULT 5  
US-10-234-406-6  
; Sequence 6, Application US/10234406  
; Publication No. US20030109478A1  
; GENERAL INFORMATION:  
; APPLICANT: FEWEL, Jason G.  
; APPLICANT: MACLAUGHLIN, Fiona  
; APPLICANT: SMITH, Louis C.  
; APPLICANT: NICOL, Francois  
; APPLICANT: ROLLAND, Alain  
; TITLE OF INVENTION: NUCLEIC ACID FORMULATIONS FOR GENE DELIVERY AND METHODS OF USE  
; FILE REFERENCE: 54964,8303,US01  
; CURRENT APPLICATION NUMBER: US/10/234,406  
; CURRENT FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/187,236  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: US 60/261,751  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: PCT/US01/06953  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Expression plasmid pFN0945 having natural sequence encoding hu  
; OTHER INFORMATION: coagulation factor IX  
US-10-234-406-6

Query Match 39.5%; Score 1039.5; DB 15; Length 461;  
Best Local Similarity 44.8%; Pred. No. 4.4e-79;  
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

QY 9 LLSASLAGLLGGE-SLFIRREOANNILARVTRANS-FLEEMKKGHLERECMEETSCEE 66  
DB 14 LITICLLGYLLSAECTVFLDHENANKILNRPKNYSKLEEFVQGNLERECMEEKCSFEE 73  
QY 67 AREVFEDSDKTNEFWNKYKDGOCETSPQONQCKDKGLGEYCTCTCLEGFEKGNCELFTFR 126  
DB 74 AREVFENTERTEFWKQYVDGQCESNCLNGSGCKDDINSYECWCPFGFEKGNCELVD- 132  
QY 127 KLCSLDNGDCQDFC-HEEQNSVVCSCARGYTLDNGKACIPTGYPGCGKOTLERKRSVA 185  
DB 133 -TCNKNRGCEQFCCKNSADNKVVCSTEGYRLAENQKSCPEAVPPFCGRVSVSQ---TS 187  
QY 186 QATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNLTRIVGGQCKDGE 245



NAME: Ausehus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 20695D-000900US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-10-348 504-44

Query Match 100.0%; Score 2634; DB 12; Length 488;  
Best Local Similarity 100.0%; Pred. No. 5.9e-213;  
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGRPLHLVLLSASLAGLLLGESLFIRREANNILARVTRANSFLEEMKKGHLERECMEE 60  
Db 1 MGRPLHLVLLSASLAGLLLGESLFIRREANNILARVTRANSFLEEMKKGHLERECMEE 60  
QY 61 TCSYEAREVPEDSDKTNEFWNKYKDGQDQETSPCQNOGCKDGLGEGYTCCTLEGFEKN 120  
Db 61 TCSYEAREVPEDSDKTNEFWNKYKDGQDQETSPCQNOGCKDGLGEGYTCCTLEGFEKN 120  
QY 121 CELTRKLSLNDGDCDQFCHEEONSVCSCARGYTLADNGKACIPGYPCKQKTLERR 180  
Db 121 CELTRKLSLNDGDCDQFCHEEONSVCSCARGYTLADNGKACIPGYPCKQKTLERR 180  
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDNQTPGERDNNLFRIVGGQE 240  
Db 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDNQTPGERDNNLFRIVGGQE 240  
QY 241 CKDCECPWQALLINEENEGCGGTILSEFYILTAACHLYQAKRFKVRVGRNTEQEBEGE 300  
Db 241 CKDCECPWQALLINEENEGCGGTILSEFYILTAACHLYQAKRFKVRVGRNTEQEBEGE 300  
QY 301 AVHEVEVVIKHNRTKTYDFDIAVLRLKTPITFRMNVAPACLPEDWAESTLMTQKTI 360  
Db 301 AVHEVEVVIKHNRTKTYDFDIAVLRLKTPITFRMNVAPACLPEDWAESTLMTQKTI 360  
QY 361 VSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 420  
Db 361 VSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 420  
QY 421 GPHVTRKDYFYVTGIVSWGESCARKGYGIYTKVTAFLKWDIRSMKTRGLPKAKSHAPE 480  
Db 421 GPHVTRKDYFYVTGIVSWGESCARKGYGIYTKVTAFLKWDIRSMKTRGLPKAKSHAPE 480  
QY 481 VITSSPLK 488  
Db 481 VITSSPLK 488

RESULT 2  
US-09-884 901-3  
Sequence 3, Application US/09884901  
Patent No. US20020076798A1  
GENERAL INFORMATION:  
APPLICANT: Miao, Carol  
APPLICANT: Kay, Mark  
TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use  
FILE REFERENCE: UOEW-1-17396  
CURRENT APPLICATION NUMBER: US/09/884,901  
PRIOR FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: US 60/212,902  
PRIOR FILING DATE: 2000-06-20  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 3  
LENGTH: 461  
TYPE: PRT  
ORGANISM: HomoSapien  
US-09-884-901-3

Query Match 39.5%; Score 1041.5; DB 9; Length 461;  
Best Local Similarity 44.8%; Pred. No. 3e-79;  
Matches 208; Conservative 76; Mismatches 157; Indels 23; Gaps 10;

QY 9 LLSASLAGLLLG-SLFIRREANNILARVTRANS-FLEEMKKGHLERECMEETCSYEE 66  
Db 14 LITICLLGYSAAECTVLDHENANKILNRPKNYSKLEEFVQGNLERECMEKCSSEE 73  
QY 67 AREVFEDSDKTNEFWNKYKDGQDQETSPCQNOGCKDGLGEGYTCCTLEGFEKNCLELFT 126  
Db 74 AREVFENTERTEFWNKQYVDGDCESNCLNGSGCKDDINSYECWCPFGFKGKNCLELDV- 132  
QY 127 KLSLDNGDCDQFC-HEEONSVCSCARGYTLADNGKACIPGYPCKQKTLERRKRSVA 185  
Db 133 -TCNINGRCEQFCNSADNKVVCSTEGYRLAENQKSCPAVPEPCGRVSVSQ----TS 187  
QY 186 QATSSSGEAPDSITWKPYDAADLDPTENPFDLLDNQTPGERDNNLFRIVGGQCKDGE 245  
Db 188 KLTRAEPVFPD-----VDYVNSTEAETILD-----NITQSTQSFNDFTRVVGEGDAKPGQ 237  
QY 246 CPWQALLINEENEGCGGTILSEFYILTAACHLYQAKRFKVRVGRNTEQEBEGEAVHEV 305  
Db 238 FWOVVL-NGKVDACGGSIVNEKMLVTAACHVETGVKITVYVAGHNIEETHTQKRN 296  
QY 306 EVVIKHNRTK--ETYDFDIAVLRLKTPITFRMNVAPACLPEDWAESTLMTQKTIYVSG 363  
Db 297 IRIIPHNNYNAINKYNHDIALLLEDEPLVLSYVTPICIADEYK-NIFLKFSGSYVSG 355  
QY 364 FGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 423  
Db 356 WGRVPHKRSALVLYRPLVDRLATCLSTRKTYNNMFCAGFHEGGRDSCQDGS 415  
QY 424 VTRFKDYFYVTGIVSWGESCARKGYGIYTKVTAFLKWDIRSMK 467  
Db 416 VTEVEGTSPLTGLISWGECEAMKGYGIYTKVSRVYVNIKEKTK 459

RESULT 3  
US-10-234-406-8  
Sequence 8, Application US/10234406  
Publication No. US20030109478A1  
GENERAL INFORMATION:  
APPLICANT: FEWEL, Jason G.  
APPLICANT: MACLAUGHLIN, Fiona  
APPLICANT: SMITH, Louis C.  
APPLICANT: NICOL, Francois  
APPLICANT: ROLLAND, Alain  
TITLE OF INVENTION: NUCLEIC ACID FORMULATIONS FOR GENE DELIVERY AND METHODS OF USE  
FILE REFERENCE: 54964.8303.US01  
CURRENT APPLICATION NUMBER: US/10/234,406  
CURRENT FILING DATE: 2002-09-03  
PRIOR APPLICATION NUMBER: US 60/187,236  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: US 60/261,751  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: PCT/US01/06953  
PRIOR FILING DATE: 2001-03-02  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Expression plasmid pFNL645 having codon optimized sequence enc  
OTHER INFORMATION: ng for human coagulation factor IX (786) ... (2171).  
US-10-234-406-8





LOCATION: 59..64  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 79..95  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 160  
OTHER INFORMATION: /note= "Disulfide linkage to  
OTHER INFORMATION: residue 132 of SEQ ID NO:2"  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 208..222  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 233..261  
US-08-330/978-1

Query Match 61.9%; Score 1631; DB 1; Length 306;  
Best Local Similarity 99.7%; Pred. No. 2.8e-123;  
Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 SVAQATSSSGEAPDSITWKPYDAADLPTENPFDLLDFNQTPERGDNNLTRIVGGQECK 242  
DB 1 SVAQATSSSGEAPDSITWKPYDAADLPTENPFDLLDFNQTPERGDNNLTRIVGGQECK 60  
QY 243 DGECPWQALLINEENEGCGGTILSEFYILTAHCLYQAKRFKRVVGRDNTQEEGEAV 302  
DB 61 DGECPWQALLINEENEGCGGTILSEFYILTAHCLYQAKRFKRVVGRDNTQEEGEAV 120  
QY 303 HEVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKTGIVS 362  
DB 121 HEVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKTGIVS 180  
QY 363 GFGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGP 422  
DB 181 GFGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGP 240  
QY 423 HVTRFKDTYFTVGTIVSWGECARKGYIKYTKVTAFLKWDIDRSMKTRGLPKAKSHAPEVI 482  
DB 241 HVTRFKDTYFTVGTIVSWGECARKGYIKYTKVTAFLKWDIDRSMKTRGLPKAKSHAPEVI 300  
QY 483 TSSPLK 488  
DB 301 TSSPLK 306

RESULT 15  
US-08-474/042-1  
Sequence 1, Application US/08474042  
Patent No. 5589572  
GENERAL INFORMATION:  
APPLICANT: King, Robert  
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED  
TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,042  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,558

FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2803-0007.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)887-1500  
TELEFAX: (202)822-0168  
TELEX: 90-4030 MBSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 306 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 59..64  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 79..95  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 160  
OTHER INFORMATION: /note= "Disulfide linkage to  
OTHER INFORMATION: residue 132 of SEQ ID NO:2"  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 208..222  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 233..261  
US-08-474-042-1

Query Match 61.9%; Score 1631; DB 1; Length 306;  
Best Local Similarity 99.7%; Pred. No. 2.8e-123;  
Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 SVAQATSSSGEAPDSITWKPYDAADLPTENPFDLLDFNQTPERGDNNLTRIVGGQECK 242  
DB 1 SVAQATSSSGEAPDSITWKPYDAADLPTENPFDLLDFNQTPERGDNNLTRIVGGQECK 60  
QY 243 DGECPWQALLINEENEGCGGTILSEFYILTAHCLYQAKRFKRVVGRDNTQEEGEAV 302  
DB 61 DGECPWQALLINEENEGCGGTILSEFYILTAHCLYQAKRFKRVVGRDNTQEEGEAV 120  
QY 303 HEVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKTGIVS 362  
DB 121 HEVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKTGIVS 180  
QY 363 GFGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGP 422  
DB 181 GFGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGP 240  
QY 423 HVTRFKDTYFTVGTIVSWGECARKGYIKYTKVTAFLKWDIDRSMKTRGLPKAKSHAPEVI 482  
DB 241 HVTRFKDTYFTVGTIVSWGECARKGYIKYTKVTAFLKWDIDRSMKTRGLPKAKSHAPEVI 300  
QY 483 TSSPLK 488  
DB 301 TSSPLK 306

Search completed: August 11, 2003, 10:29:58  
Job time : 32 secs

Db 242 ECECPWQALLVNEENEGCGTILNEFYVLTAAHCLHQAKRFTVRVGRNTEQEGNEMA 301  
QY 303 HEVEVVIKHNFTKTYDDEDFIAVLRLKTPITFRMNVAPACLPEDWAEATLMTQKTGIVS 362  
Db 302 HEVEMTKHRSFVAKETDDEDFIAVLRLKTPITFRMNVAPACLPEDWAEATLMTQKTGIVS 361  
QY 363 GFGRTHKGROSTRKLMLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGGP 422  
Db 362 GFGRTHKGRLSSTLKMLEVPYVDNRSTCKLSSSFTITPNMFCAGYDTQPEDACQDGGGP 421  
QY 423 HVTFRKDTYFTVGTIVSGESCARKGKIYTKVTAFLKWIDRSMKTR-GLPKAKSHA 478  
Db 422 HVTFRKDTYFTVGTIVSGESCARKGKIYTKVSNFLKWIDKIMKARAGAAGSRGHS 478

## RESULT 13

US-08-469-658-53  
; Sequence 53, Application US/08469658  
; Patent No. 5917018  
; GENERAL INFORMATION:  
; APPLICANT: Th egersen, Hans Christian  
; APPLICANT: Holtet, Thor Las  
; APPLICANT: Etzerodt, Michael  
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02110-2804

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version  
; SOFTWARE: #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,658  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/192,060  
; FILING DATE: February 4, 1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 06363/002002

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617 542 5070  
; TELEFAX: 617 542 8906  
; TELEX: 200154

INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-469-658-53

Query Match 70.1%; Score 1847; DB 2; Length 487;  
Best Local Similarity 70.4%; Pred. No. 2.4e-140;  
Matches 336; Conservative 59; Mismatches 76; Indels 6; Gaps 3;

QY 5 LHLVLLSASLAGLLGLSFLIRREQANNILARYTRANSFLEEMKKGHLRECEMEETCSY 64  
Db 5 LHLVLLSALGGLLRPGASVFLPDAQHRVLRARRANSFLEEVKQGNLERECLEACSL 64

QY 65 EEAREVFEDSKTNEFNWYKDGDOCTSPCONQCKCKGLGEYTCCTCLEGPEGKNCBLF 124  
Db 65 EEAREVFEDAEQTDDEFWSKYKDGQCEGHPCLNQGHCKDGIQDYTCACBEGEGNCEFS 124  
QY 125 TRKLSLNDGDCDDQCCHBEQNSVSCARGYTYLANDKACIPTGYPGCKGTFLERRKRSV 184  
Db 125 TREICSLNDGDCDDQCFREERSEVRSCAHGYVGLDDSKSCVSTERFPCGKETQGRSRR-- 182  
QY 185 AQTSSSGAPDSITWKPYDAADLPDENPFDLPNOTPERGD--NNLTFRIVGGQRC 242  
Db 183 -WAIHTSEDALDALEHYDPADLSFTSSLDLGLNRTPEPSAGEDGGQVVRIVGRUCA 241  
QY 243 DGECPWQALLVNEENEGFCGGTILSEFYILTAAHCLYQAKRFKRVGRNTEQEGGSAV 302  
Db 242 ECECPWQALLVNEENEGFCGGTILNEFYVLTAAHCLHQAKRFTVRVGRNTEQEGNEMA 301  
QY 303 HEVEVVIKHNFTKTYDDEDFIAVLRLKTPITFRMNVAPACLPEDWAEATLMTQKTGIVS 362  
Db 302 HEVEMTKHRSFVAKETDDEDFIAVLRLKTPITFRMNVAPACLPEDWAEATLMTQKTGIVS 361  
QY 363 GFGRTHKGROSTRKLMLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGGGP 422  
Db 362 GFGRTHKGRLSSTLKMLEVPYVDNRSTCKLSSSFTITPNMFCAGYDTQPEDACQDGGGP 421  
QY 423 HVTFRKDTYFTVGTIVSGESCARKGKIYTKVTAFLKWIDRSMKTR-GLPKAKSHA 478  
Db 422 HVTFRKDTYFTVGTIVSGESCARKGKIYTKVSNFLKWIDKIMKARAGAAGSRGHS 478

## RESULT 14

US-08-330-978-1  
; Sequence 1, Application US/08330978  
; Patent No. 5589571  
; GENERAL INFORMATION:  
; APPLICANT: King, Robert  
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED  
; TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 2000 Pennsylvania Avenue, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,978  
; FILING DATE: 28-OCT-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,558  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2803-0007.02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)887-1500  
; TELEFAX: (202)822-0168  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 306 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE: Disulfide-bond

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Db      482 ATWTVPP 488
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RESULT 12
US-08-469-486-53
; Sequence 53, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thøgersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Ezerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paul T. Clark
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 06363/002001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617 542 5070
/ TELEFAX: 617 542 8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 487 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-469-486-53

Query Watch 70.1%; Score 1847; DB 1; Length 487;
Best Local Similarity 70.4%; Pred. No. 2.4e-140;
Matches 336; Conservative 59; Mismatches 76; Indels 6; Gaps 3;

QY 5 LHLVILSASLAGLLLGESLFIIRCOANNILARVTRANSFLERMKKGHLERECMEETCSY 64
Db 5 LHLVLLSTALGRLPAGSVFLPRQAHKVRQARRANSFLVEVKOGNLERECLEERCSL 64

QY 65 EEARVFEFDSKTNFWNKYKDGQOCETSPCONQKCKDGLGEYTCITCLEGFEGKNCELF 124
Db 65 EEARVFEFDEAQTDEFSKYKDGQCEGHPCLNQGHCKDGDYDCTCAEGFEGKNCEFS 124

QY 125 TKRLCSLDNGDCDQCFHEBQNSVWCSCARGYTLADNGKACIPTGPYPCGKQTLERKRVS 184
Db 125 TREICSLDNGGCDQFCREERSEVRCSAHGYVLGDDSKSCVSTERFPCKGFTQGRSRR-- 182

QY 185 AQATSSSGEAPDSITWKPYDAADLPDENPFDLLDFNQTPQPERGD--NNLTRIVGGQECK 242
Db 183 -WAIITSEADALDASELHYDPAIDLPTSESLDLLGLNLTPEPSAGDGSQVVRIGRDC 241

QY 243 DCECPWOALLINEENEGFCGGTILSEFYLTAAHCLYQAKRFKVRVGRDNTBOEGGEAV 302

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LOCATION: 299..313, 324..352)  
US-08-4877037-3

Query Match 85.18; Score 2241.5; DB 1; Length 437;  
Best Local Similarity 86.58; Pred. No. 4.9e-172;  
Matches 422; Conservative 2; Mismatches 13; Indels 51; Gaps 1;

QY 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLBEMKKGHLRECEMEE 60  
DB 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLBEMKKGHLRECEMEE 60  
QY 61 TCSYEAREVPEDSDKTNFNNKYKDGQOCETSPCQNGKCKDGLGEYTCCTCLEGFEKN 120  
DB 61 TCSYTTARTFTSDKTNFNNKYKDGQOCETSPCQNGKCKDGLGEYTCCTCLEGFEKN 120  
QY 121 CELFTRKLSLDNGDCDFCHEEQNSVVCSCARGYTLADNGKACIPTGPPCKQTLERR 180  
DB 121 CELFTRKLSLDNGDCDFCHEEQNSVVCSCARGYTLADNGKACIPTGPPCKQTLERR 180  
QY 181 KRSVAQATSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTPGERGNNLRIYVGQE 240  
DB 181 KR-----RIVGQE 189  
QY 241 CKGECQWALLINEEGFCGTTILSEFYILTAACHLYOAKRFKRVGDRNTEQEGGE 300  
DB 190 CKGECQWALLINEEGFCGTTILSEFYILTAACHLYOAKRFKRVGDRNTEQEGGE 249  
QY 301 AVHEVEVVIKHNFTKETYDFDIIVLRLKTPITFRMNVAPACLPEDMAESTLMTOKGI 360  
DB 250 AVHEVEVVIKHNFTKETYDFDIIVLRLKTPITFRMNVAPACLPEDMAESTLMTOKGI 309  
QY 361 VSGFGRTHKGROSTRKMLEVYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACOGDSG 420  
DB 310 VSGFGRTHKGROSTRKMLEVYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACOGDSG 369  
QY 421 GPHVTRFKDITYFTVIGVSWGECGARKGYIKYTKVAFKLWIDRSMKTRGLPKAKSHAPE 480  
DB 370 GPHVTRFKDITYFTVIGVSWGECGARKGYIKYTKVAFKLWIDRSMKTRGLPKAKSHAPE 429  
QY 481 VITSSPLK 488  
DB 430 VITSSPLK 437

RESULT 10  
US-08-469-486-2  
; Sequence 2, Application US/08469486  
; Patent No. 5739281  
; GENERAL INFORMATION:  
; APPLICANT: Thøgersen, Hans Christian  
; APPLICANT: Holtet, Thor Las  
; APPLICANT: Etzerodt, Michael  
; TITLE OF INVENTION: Improved method for the refolding of  
; TITLE OF INVENTION: proteins  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,486  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:

RESULT 11  
US-08-469-658-2  
; Sequence 2, Application US/08469658  
; Patent No. 5917018  
; GENERAL INFORMATION:  
; APPLICANT: Thøgersen, Hans Christian  
; APPLICANT: Holtet, Thor Las  
; APPLICANT: Etzerodt, Michael  
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.

APPLICATION NUMBER: 08/192,060  
FILING DATE: February 4, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 06363/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617 542 5070  
TELEFAX: 617 542 8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-486-2

Query Match 70.3%; Score 1851; DB 1; Length 492;  
Best Local Similarity 69.8%; Pred. No. 1.1e-140;  
Matches 340; Conservative 58; Mismatches 81; Indels 8; Gaps 4;  
QY 5 LHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLBEMKKGHLRECEMEECSY 64  
DB 5 LHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLBEMKKGHLRECEMEECSY 64  
QY 65 BEARVFEEDSDKTNFNNKYKDGQOCETSPCQNGKCKDGLGEYTCCTCLEGFEKNCELF 124  
DB 65 BEARVFEEDSDKTNFNNKYKDGQOCETSPCQNGKCKDGLGEYTCCTCLEGFEKNCELF 124  
QY 125 TRKLSLDNGDCDFCHEEQNSVVCSCARGYTLADNGKACIPTGPPCKQTLERRKRSV 184  
DB 125 TRKLSLDNGDCDFCHEEQNSVVCSCARGYTLADNGKACIPTGPPCKQTLERRKRSV 184  
QY 185 AQATSSSSEAPDSITWKPYDAADLDPTENPFDLLDFNQTPGERG--NNLRIYVGGECK 242  
DB 183 -WAHTSDALDASELEHYDPADLSPTESSLDLLGLNRTPEAGEDSGSVVRIYVGRDCA 241  
QY 243 DGECPWQALLINEEGFCGTTILSEFYILTAACHLYOAKRFKRVGDRNTEQEGSEAV 302  
DB 242 DGECPWQALLINEEGFCGTTILSEFYILTAACHLYOAKRFKRVGDRNTEQEGSEAV 301  
QY 303 HEVEVVIKHNFTKETYDFDIIVLRLKTPITFRMNVAPACLPEDMAESTLMTOKTIGVS 362  
DB 302 HEVEVVIKHNFTKETYDFDIIVLRLKTPITFRMNVAPACLPEDMAESTLMTOKTIGVS 361  
QY 363 GFGTRTHKGROSTRKMLEVYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACOGDSGGP 422  
DB 362 GFGTRTHKGROSTRKMLEVYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACOGDSGGP 421  
QY 423 HVTRFKDITYFTVIGVSWGECGARKGYIKYTKVAFKLWIDRSMKTR-GLPKAKSH--AP 479  
DB 422 HVTRFKDITYFTVIGVSWGECGARKGYIKYTKVAFKLWIDRSMKTR-GLPKAKSH--AP 479  
QY 480 EVITSSP 486  
DB 482 ATWTVPP 488

LOCATION: 84  
OTHER INFORMATION: /note= "Location of Intron D"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 128  
OTHER INFORMATION: /note= "Location of Intron E"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: (158-159)  
OTHER INFORMATION: /note= "Location of Intron F"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 198  
OTHER INFORMATION: /note= "Location of Intron G"  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96  
LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,  
LOCATION: 299..313, 324..352)  
US-08-4871037-2

Query Match 85.4%; Score 2249.5; DB 1; Length 437;  
Best Local Similarity 86.9%; Pred. No. le-172;  
Matches 424; Conservative 0; Mismatches 13; Indels 51; Gaps 1;

QY 1 MGRPLHLVLSASLAGLLLGESLFIIRQANNILARVTRANSFLTEEMKKGHLEECMEE 60  
DB 1 MGRPLHLVLSASLAGLLLGESLFIIRQANNILARVTRANSFLTEEMKKGHLEECMEE 60  
QY 61 TCSYEAREVFEDSDKTNEFWNKYKDGQCETSPCONQCKDGLGEYTCCTLEGPEGN 120  
DB 61 TCSYTTARTVFTSDKTNEFWNKYKDGQCETSPCONQCKDGLGEYTCCTLEGPEGN 120  
QY 121 CELFTRKLCSLDNGCDQFCHERQNSVVCSCARGYTLADNGKACIPTGYPCKQTLERR 180  
DB 121 CELFTRKLCSLDNGCDQFCHERQNSVVCSCARGYTLADNGKACIPTGYPCKQTLERR 180  
QY 181 KRSVAQATSSGEAPDSITWKPYDAADLPDENPFDLLDFNQTPQPERGNNLTRIVGGQE 240  
DB 181 KR-----RIVGGQE 189  
QY 241 CKGCECPWQALLNEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEEGE 300  
DB 190 CKDCECPWQALLNEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEEGE 249  
QY 301 AVHEVEVVIKHNRTKETDYDFDIARLRLKTPITFRMNVAPACLPEDWAEESTLMTQGTI 360  
DB 250 AVHEVEVVIKHNRTKETDYDFDIARLRLKTPITFRMNVAPACLPEDWAEESTLMTQGTI 309  
QY 361 VSGFGRTHRGQSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 420  
DB 310 VSGFGRTHRGQSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 369  
QY 421 GPHVTRFKDYFYVTGIVSWGECARCKYGIYTKVTAFLKWIIDRSMTKRLPLKAKSHAPE 480  
DB 370 GPHVTRFKDYFYVTGIVSWGECARCKYGIYTKVTAFLKWIIDRSMTKRLPLKAKSHAPE 429  
QY 481 VITSSPLK 488  
DB 430 VITSSPLK 437

RESULT 9  
US-08-4871037-3  
; Sequence 3, Application US/08487037  
; Patent No. 5795863  
; GENERAL INFORMATION:  
; APPLICANT: Wolf, David L.  
; TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,037  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0002.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 437 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: -40...397  
OTHER INFORMATION: /note= "Same features apply from  
OTHER INFORMATION: SEQ ID NO:2"  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..139  
OTHER INFORMATION: /note= "Factor Xa - Light Chain"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: -40..0  
OTHER INFORMATION: /note= "Pre-Pro leader sequence"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: -17  
OTHER INFORMATION: /note= "Location of Intron A"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: (37-38)  
OTHER INFORMATION: /note= "Location of Intron B"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 46  
OTHER INFORMATION: /note= "Location of Intron C"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 63  
OTHER INFORMATION: /note= "An amino acid represented  
OTHER INFORMATION: by the greek letter Beta"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 84  
OTHER INFORMATION: /note= "Location of Intron D"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: (158-159)  
OTHER INFORMATION: /note= "Location of Intron F"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 198  
OTHER INFORMATION: /note= "Location of Intron G"  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96  
LOCATION: ..109, 111..124, 132..251, 150..155, 170..186,



```

COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC0472P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYDROPHETICAL: NO
ANTISENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..139
OTHER INFORMATION: /note= "Factor X Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 140..142
OTHER INFORMATION: /note= "Factor X Connecting"
OTHER INFORMATION: Tripeptide"
FEATURE:
NAME/KEY: Region
LOCATION: 143..448
OTHER INFORMATION: /note= "Factor X Heavy Chain"
PCT-US92-10242-3

Query Match
Best Local Similarity 92.6%; Score 2439; DB 5; Length 448;
Matches 446; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 ANSLEEMKKHGLERECHEETCSYEAREVFEDSDKTNEFWNKYKDGQDQETSPQONQK 100
DB 1 ANSLEEMKKHGLERECHEETCSYEAREVFEDSDKTNEFWNKYKDGQDQETSPQONQK 60
QY 101 CKDGLGEYTCCLGEGFKNCLELFTRLKSLDNGDCDQFCHEQNSVVCSCARGYTLADN 160
DB 61 CKBGLGEYTCCLGEGFKNCLELFTRLKSLDNGDCDQFCHEQNSVVCSCARGYTLADN 120
QY 161 GKACIPGTPYCGKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDF 220
DB 121 GKACIPGTPYCGKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDF 180
QY 221 NOTOPRGDNNLTIRIVGQCKGCECPWQALLNEENEGCGGTILSEFYILAAHCLYQ 280
DB 181 NOTOPRGDNNLTIRIVGQCKGCECPWQALLNEENEGCGGTILSEFYILAAHCLYQ 240
QY 281 AKRFKVRGDRNTQEGEGGAVHEVVIKHNFTKTYDFDIKLVRLKTPITFRNVAP 340
DB 241 AKRFKVRGDRNTQEGEGGAVHEVVIKHNFTKTYDFDIKLVRLKTPITFRNVAP 300
QY 341 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRSTRKMLKLEVPYVDRNSCKLSSFFITQ 400
DB 301 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRSTRKMLKLEVPYVDRNSCKLSSFFITQ 360
QY 401 NMFCAGYDTKQEDACQDGGPHVTRFKDTYFTVGTIVSGECARCKGKIYTKVTAFLK 460

Db 361 NMFCAGYDTKQEDACQDGGPHVTRFKDTYFTVGTIVSGECARCKGKIYTKVTAFLK 420
QY 461 WIDRSMKTRGLPKAKSHAPEVITSSPLK 488
DB 421 WIDRSMKTRGLPKAKSHAPEVITSSPLK 448

RESULT 8
US-08-487-037-2
; Sequence 2, Application US/08487037
; Patent No. 5795863
; GENERAL INFORMATION:
; APPLICANT: Wolf, David L.
; TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,037
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0002.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..139
; OTHER INFORMATION: /note= "Factor Xa-Light Chain"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: -40..0
; OTHER INFORMATION: /note= "Pre-Pro leader sequence"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: -17
; OTHER INFORMATION: /note= "Location of Intron A"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: (37-38)
; OTHER INFORMATION: /note= "Location of Intron B"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 46
; OTHER INFORMATION: /note= "Location of Intron C"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 63
; OTHER INFORMATION: /note= "An amino acid represented
; OTHER INFORMATION: by the greek letter Beta"
; FEATURE:
; NAME/KEY: Modified-site
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Db 1 ANSFLEEMKKGHLERECMEETCSYEAREVFEDSKTNEFWNKYKDGQDQETSPCQNOGK 60  
QY 101 CKDGLGEYTCCTLEGEGKNCLEFTRKLCSLDNGDCDOFCHEEONSVCSCARGYTLADN 160  
Db 61 CKBGLGEYTCCTLEGEGKNCLEFTRKLCSLDNGDCDOFCHEEONSVCSCARGYTLADN 120  
QY 161 GRACIPTGPGCGKQTLERRKRSVAQATSSGEAPDSITWKPYDAADLDPTENPFDLLDF 220  
Db 121 GRACIPTGPGCGKQTLERRKRSVAQATSSGEAPDSITWKPYDAADLDPTENPFDLLDF 180  
QY 221 NQTPERGNNLTRIVGQCKGECPCWQALLINEENEGFCGGTILSEFYILTAHCLYQ 280  
Db 181 NQTPERGNNLTRIVGQCKGECPCWQALLINEENEGFCGGTILSEFYILTAHCLYQ 240  
QY 281 AKRFKVRGDRNTEQEGEGEAHVEVVKHNRTKETDYDFDIAVLRLKTPITFRMNVAP 340  
Db 241 AKRFKVRGDRNTEQEGEGEAHVEVVKHNRTKETDYDFDIAVLRLKTPITFRMNVAP 300  
QY 341 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVYPYVDRNSCKLSSFFIITQ 400  
Db 301 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVYPYVDRNSCKLSSFFIITQ 360  
QY 401 NMFAGYDTKQEDACQDGGSPHVTFRKDYTFVTGIVSWGESCARKGYIYTKVTAFLK 460  
Db 361 NMFAGYDTKQEDACQDGGSPHVTFRKDYTFVTGIVSWGESCARKGYIYTKVTAFLK 420  
QY 461 WDRSMKTRGLPKAKSHAPEVITSSPLK 488  
Db 421 WDRSMKTRGLPKAKSHAPEVITSSPLK 448

RESULT 6  
US-08-955-471-3  
; Sequence 3, Application US/08955471  
; Patent No. 5968751  
; GENERAL INFORMATION:  
; APPLICANT: Griffin, John H.  
; APPLICANT: Mesters, Rolf M.  
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
; TITLE OF INVENTION: for Inhibiting Coagulation  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Office of Patent Counsel, The Scripps  
; ADDRESSEE: Research Institute  
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/955,471  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/295,411  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSRI263.0C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 448 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..139  
OTHER INFORMATION: /note= "Factor X Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 140..142  
OTHER INFORMATION: /note= "Factor X Connecting  
OTHER INFORMATION: Tripeptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 143..448  
OTHER INFORMATION: /note= "Factor X Heavy Chain"  
US-08-955-471-3  
Query Match 92.6%; Score 2439; DB 2; Length 448;  
Best Local Similarity 99.6%; Pred. No. 6,6e-188;  
Matches 446; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 41 ANSFLEEMKKGHLERECMEETCSYEAREVFEDSKTNEFWNKYKDGQDQETSPCQNOGK 100  
Db 1 ANSFLEEMKKGHLERECMEETCSYEAREVFEDSKTNEFWNKYKDGQDQETSPCQNOGK 60  
QY 101 CKDGLGEYTCCTLEGEGKNCLEFTRKLCSLDNGDCDOFCHEEONSVCSCARGYTLADN 160  
Db 61 CKBGLGEYTCCTLEGEGKNCLEFTRKLCSLDNGDCDOFCHEEONSVCSCARGYTLADN 120  
QY 161 GRACIPTGPGCGKQTLERRKRSVAQATSSGEAPDSITWKPYDAADLDPTENPFDLLDF 220  
Db 121 GRACIPTGPGCGKQTLERRKRSVAQATSSGEAPDSITWKPYDAADLDPTENPFDLLDF 180  
QY 221 NQTPERGNNLTRIVGQCKGECPCWQALLINEENEGFCGGTILSEFYILTAHCLYQ 280  
Db 181 NQTPERGNNLTRIVGQCKGECPCWQALLINEENEGFCGGTILSEFYILTAHCLYQ 240  
QY 281 AKRFKVRGDRNTEQEGEGEAHVEVVKHNRTKETDYDFDIAVLRLKTPITFRMNVAP 340  
Db 241 AKRFKVRGDRNTEQEGEGEAHVEVVKHNRTKETDYDFDIAVLRLKTPITFRMNVAP 300  
QY 341 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVYPYVDRNSCKLSSFFIITQ 400  
Db 301 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVYPYVDRNSCKLSSFFIITQ 360  
QY 401 NMFAGYDTKQEDACQDGGSPHVTFRKDYTFVTGIVSWGESCARKGYIYTKVTAFLK 460  
Db 361 NMFAGYDTKQEDACQDGGSPHVTFRKDYTFVTGIVSWGESCARKGYIYTKVTAFLK 420  
QY 461 WDRSMKTRGLPKAKSHAPEVITSSPLK 488  
Db 421 WDRSMKTRGLPKAKSHAPEVITSSPLK 448

RESULT 7  
PCT-US92-10242-3  
; Sequence 3, Application PC/TUS9210242  
; GENERAL INFORMATION:  
; APPLICANT: Griffin, John H.  
; APPLICANT: Mesters, Rolf  
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
; TITLE OF INVENTION: for Inhibiting Coagulation  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Office of Patent Counsel, The Scripps  
; ADDRESSEE: Research Institute  
; STREET: 10666 North Torrey Pines Road, TPC 8  
; CITY: La Jolla  
; STATE: CA

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10068  
FILING DATE: 19921120  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/798,221  
FILING DATE: 22-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: SCR1221P  
REFERENCE/DOCKET NUMBER: 34,163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 448 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..139  
OTHER INFORMATION: /note= "Factor X Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 140..142  
OTHER INFORMATION: /note= "Factor X Connecting  
OTHER INFORMATION: Tripeptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 143..448  
OTHER INFORMATION: /note= "Factor X Heavy Chain"  
PCT-US92-10068-1

Query Match 92.7%; Score 2441; DB 5; Length 448;  
Best Local Similarity 99.8%; Pred. No. 4.5e-188;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 ANSFLEEMKKGHLRECEMEETCSYEAREVFEDSDKTNEFWNKYKGDQCETSPCQNOGK 100  
DB 1 ANSFLEEMKKGHLRECEMEETCSYEAREVFEDSDKTNEFWNKYKGDQCETSPCQNOGK 60  
QY 101 CKDGLGYTCCTCLEGFGKNCLEFTRKLCSLDNGDCDQFCHEQNSVVCSCARGYTLADN 160  
DB 61 CKDGLGYTCCTCLEGFGKNCLEFTRKLCSLDNGDCDQFCHEQNSVVCSCARGYTLADN 120  
QY 161 GKACIPTGYPYCGKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDF 220  
DB 121 GKACIPTGYPYCGKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDF 180  
QY 221 NOTOPERGDNLLTRIVGQCKGDCGCPWQALLINEEGFCGGTILSEFYILTAACHLYQ 280  
DB 181 NOTOPERGDNLLTRIVGQCKGDCGCPWQALLINEEGFCGGTILSEFYILTAACHLYQ 240  
QY 281 AKREKVRVGRDNTQEGEGGAHVVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAP 340  
DB 241 AKREKVRVGRDNTQEGEGGAHVVEVVIKHNRTKETYDFDIAVLRLKTPITFRMNVAP 300  
QY 341 ACLPERDWAESTLMTQKTIGVSGFGRTHKGRGSTRKLMLEVPYVDNRNSKLSSSFIITQ 400  
DB 301 ACLPERDWAESTLMTQKTIGVSGFGRTHKGRGSTRKLMLEVPYVDNRNSKLSSSFIITQ 360  
QY 401 NMFACAGYDTQEDACQDGGPHVTRFKDYFTVGTIVSGEACARKGKYGIYTKVTAFLK 460  
DB 361 NMFACAGYDTQEDACQDGGPHVTRFKDYFTVGTIVSGEACARKGKYGIYTKVTAFLK 420

QY 461 WIDRSMKTRGLPKAKSHAPEVITSSPLK 488  
DB 421 WIDRSMKTRGLPKAKSHAPEVITSSPLK 448

RESULT 5  
US-08-295-411-3  
Sequence 3, Application US/08295411  
Patent No. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Mesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI263.0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 448 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..139  
OTHER INFORMATION: /note= "Factor X Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 140..142  
OTHER INFORMATION: /note= "Factor X Connecting  
OTHER INFORMATION: Tripeptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 143..448  
OTHER INFORMATION: /note= "Factor X Heavy Chain"  
US-08-295-411-3

Query Match 92.6%; Score 2439; DB 1; Length 448;  
Best Local Similarity 99.6%; Pred. No. 6.6e-188;  
Matches 446; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 ANSFLEEMKKGHLRECEMEETCSYEAREVFEDSDKTNEFWNKYKGDQCETSPCQNOGK 100

ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,037  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0002.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: -17  
OTHER INFORMATION: /note= "Location of Intron A"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: (37-38)  
OTHER INFORMATION: /note= "Location of Intron B"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 46  
OTHER INFORMATION: /note= "Location of Intron C"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 63  
OTHER INFORMATION: /note= "Amino acid represented by the greek letter Beta"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 84  
OTHER INFORMATION: /note= "Location of Intron D"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 128  
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FEATURE:  
NAME/KEY: Modified-site  
LOCATION: (209-210)  
OTHER INFORMATION: /note= "Location of Intron F"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 249  
OTHER INFORMATION: /note= "Location of Intron G"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: -40..0  
OTHER INFORMATION: /note= "Pre-Pro leader sequence"  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..139  
OTHER INFORMATION: /note= "Factor Xa- Light chain"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 143..194

OTHER INFORMATION: /note= "Activation Peptide"  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 195..448  
OTHER INFORMATION: /note= "Factor Xa-Heavy Chain"  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96  
LOCATION: .109, 111..124, 132..302, 201..206, 221..237,  
LOCATION: 350..364, 375..403)  
US-08-487-037-1

Query Match 97.1%; Score 2557; DB 1; Length 488;  
Best Local Similarity 97.3%; Pred. No. 2.5e-197;  
Matches 475; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 1 MGRPLHLVLLSASLAGLLLLGESLFIHQEQANNILARVTRANSFLEEMKKGHLRECEMEE 60  
DB 1 MGRPLHLVLLSASLAGLLLLGESLFIHQEQANNILARVTRANSFLEEMKKGHLRECEMEE 60  
QY 61 TCSYEAREVEFEDSDKTNEFWNKYKDGDCQCTSPQNGKCKGGLGEYTCCTCLEGFEKGN 120  
DB 61 TCSYTTARTVFTDSKNTFWNKYKDGDCQCTSPQNGKCKGGLGEYTCCTCLEGFEKGN 120  
QY 121 CELFTRKLCSLDNGDCQFCHEEQNSVVCARGYTLADNGKACIPTGPGKQTLERR 180  
DB 121 CELFTRKLCSLDNGDCQFCHEEQNSVVCARGYTLADNGKACIPTGPGKQTLERR 180  
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENFDLLDFNOTOPERGDNLLTRIVGQE 240  
DB 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENFDLLDFNOTOPERGDNLLTRIVGQE 240  
QY 241 CKDGCPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDTEQEEGGE 300  
DB 241 CKDGCPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDTEQEEGGE 300  
QY 301 AVHEVEVVIKHNRTKEYDFDIAVLRLKTPITRMNVAPACLPERDWAESTLMTQKTI 360  
DB 301 AVHEVEVVIKHNRTKEYDFDIAVLRLKTPITRMNVAPACLPERDWAESTLMTQKTI 360  
QY 361 VSGFGRTHEKGROSTRKMLVPPYVDRNSCKLSSTFIITQNMFCAGYDTKQEDACQDGS 420  
DB 361 VSGFGRTHEKGROSTRKMLVPPYVDRNSCKLSSTFIITQNMFCAGYDTKQEDACQDGS 420  
QY 421 GPHVTRFKDFTYVTGIVSWGESCARKGYGYTKVTAFLKWDKIDRSMKTRGLPKAKSHAPE 480  
DB 421 GPHVTRFKDFTYVTGIVSWGESCARKGYGYTKVTAFLKWDKIDRSMKTRGLPKAKSHAPE 480  
QY 481 VITSSPLK 488  
DB 481 VITSSPLK 488

RESULT 4  
PCT-US92-10068-1  
Sequence 1, Application PC/TUS9210068  
GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C  
APPLICANT: Edgington, Thomas S  
APPLICANT: Fair, Daryl S  
TITLE OF INVENTION: Factor X-derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Inflammation  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 North Torrey Pines Road  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:

SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-09-367777-44

Query Match 100.0%; Score 2634; DB 4; Length 488;  
Best Local Similarity 100.0%; Pred. No. 1.6e-203;  
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
DB 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
QY 61 TCSYEAREVEFSDKTNEFWNKYKDGQCETSPCQNGKCKDGLGEYTCCTLEGEGKN 120  
DB 61 TCSYEAREVEFSDKTNEFWNKYKDGQCETSPCQNGKCKDGLGEYTCCTLEGEGKN 120  
QY 121 CELFTRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180  
DB 121 CELFTRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180  
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNQTQPERGDNLTTRIVGGQE 240  
DB 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNQTQPERGDNLTTRIVGGQE 240  
QY 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGGE 300  
DB 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGGE 300  
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DB 301 AVHEVEVVIKHNRTKETDYDFDIIVLRLKPTITFRMNVAPACILPERDMAESTLMTQKTI 360  
QY 361 VSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSLSSFIITQNMFCAGYDTKQEDACQGGSG 420  
DB 361 VSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSLSSFIITQNMFCAGYDTKQEDACQGGSG 420  
QY 421 GPHVTRFKDITYFTVIGVSWGESCARKKGYIYTKVTAFLKWDIRSMKTRGLPKAKSHAPE 480  
DB 421 GPHVTRFKDITYFTVIGVSWGESCARKKGYIYTKVTAFLKWDIRSMKTRGLPKAKSHAPE 480  
QY 481 VITSSPLK 488  
DB 481 VITSSPLK 488

RESULT 2  
US-09-3677791A-27  
: Sequence 27, Application US/09367791A  
: Patent No. 6573071  
: GENERAL INFORMATION:  
: APPLICANT: Himmelsbach, Michele  
: Schlokat, Uwe  
: Dörner, Friedrich  
: Fisch, Andreas  
: Eibl, Johann  
: TITLE OF INVENTION: Factor X Analogues With  
: a Modified Protease Cleavage Site  
: NUMBER OF SEQUENCES: 122  
: CORRESPONDENCE ADDRESS:  
: ADDRESS: Townsend and Townsend and Crew LLP  
: STREET: Two Embarcadero Center, Eighth Floor  
: CITY: San Francisco  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 94111-3834  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FastSeq for Windows Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/367,791A  
: FILING DATE: 12-No. 6573071-1999  
: CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AT A 335/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCT/AT98/00045  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,471  
REFERENCE/DOCKET NUMBER: 20695D-00070005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-367-791A-27

Query Match 100.0%; Score 2634; DB 4; Length 488;  
Best Local Similarity 100.0%; Pred. No. 1.6e-203;  
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
DB 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
QY 61 TCSYEAREVEFSDKTNEFWNKYKDGQCETSPCQNGKCKDGLGEYTCCTLEGEGKN 120  
DB 61 TCSYEAREVEFSDKTNEFWNKYKDGQCETSPCQNGKCKDGLGEYTCCTLEGEGKN 120  
QY 121 CELFTRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180  
DB 121 CELFTRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180  
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNQTQPERGDNLTTRIVGGQE 240  
DB 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNQTQPERGDNLTTRIVGGQE 240  
QY 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGGE 300  
DB 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVGDRNTEQEGGE 300  
QY 301 AVHEVEVVIKHNRTKETDYDFDIIVLRLKPTITFRMNVAPACILPERDMAESTLMTQKTI 360  
DB 301 AVHEVEVVIKHNRTKETDYDFDIIVLRLKPTITFRMNVAPACILPERDMAESTLMTQKTI 360  
QY 361 VSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSLSSFIITQNMFCAGYDTKQEDACQGGSG 420  
DB 361 VSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSLSSFIITQNMFCAGYDTKQEDACQGGSG 420  
QY 421 GPHVTRFKDITYFTVIGVSWGESCARKKGYIYTKVTAFLKWDIRSMKTRGLPKAKSHAPE 480  
DB 421 GPHVTRFKDITYFTVIGVSWGESCARKKGYIYTKVTAFLKWDIRSMKTRGLPKAKSHAPE 480  
QY 481 VITSSPLK 488  
DB 481 VITSSPLK 488

RESULT 3  
US-08-487-037-1  
: Sequence 1, Application US/08487037  
: Patent No. 5795863  
: GENERAL INFORMATION:  
: APPLICANT: Wolf, David L.  
: TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
: NUMBER OF SEQUENCES: 11  
: CORRESPONDENCE ADDRESS:

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OM protein - protein search, using sw model
Run on:      August 11, 2003, 10:24:44 ; Search time 30 Seconds
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              688.257 Million cell updates/sec

Title:       US-09-632-722-2
Perfect score: 2634
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Scoring table:
Gapop 10.0 , Gapext 0.5

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RESULT 1  
US-09-367-777-44  
Sequence 44, Application US/09367777  
Patent No. 6562598  
GENERAL INFORMATION:  
APPLICANT: Himmelspach, Michele  
Pfleiderer, Michael  
Falkner, Falko-Guenther  
Eibl, Johann  
Dorner, Friedrich  
Schlokot, Uwe  
TITLE OF INVENTION: Factor X Deletion Mutants  
and Analogues Thereof  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco

Result No.	Score	Query Match	Length	DB	ID	Description
1	2634	100.0	488	4	US-09-367-777-44	Sequence 44, Appl
2	2634	100.0	488	4	US-09-367-791A-27	Sequence 27, Appl
3	2557	97.1	488	1	US-08-487-037-1	Sequence 1, Appl
4	2441	92.7	448	5	PCT-US92-10068-1	Sequence 1, Appl
5	2439	92.6	448	1	US-08-235-411-3	Sequence 3, Appl
6	2439	92.6	448	2	US-08-935-471-3	Sequence 3, Appl
7	2439	92.6	448	5	PCT-US92-10242-3	Sequence 3, Appl
8	2249.5	85.4	437	1	US-08-487-037-2	Sequence 2, Appl
9	2241.5	85.1	437	1	US-08-487-037-3	Sequence 3, Appl
10	1851	70.3	492	1	US-08-489-486-2	Sequence 2, Appl
11	1851	70.3	492	2	US-08-469-658-2	Sequence 2, Appl
12	1847	70.1	487	1	US-08-469-486-53	Sequence 53, Appl
13	1847	70.1	487	2	US-08-469-658-53	Sequence 53, Appl
14	1631	61.9	306	1	US-08-330-978-1	Sequence 1, Appl
15	1631	61.9	306	1	US-08-474-042-1	Sequence 1, Appl
16	1631	61.9	306	1	US-08-484-558-1	Sequence 1, Appl
17	1631	61.9	306	1	US-08-774-592-1	Sequence 1, Appl
18	1354	51.4	254	1	US-08-330-978-3	Sequence 3, Appl
19	1354	51.4	254	1	US-08-474-042-3	Sequence 3, Appl
20	1354	51.4	254	1	US-08-484-558-3	Sequence 3, Appl
21	1354	51.4	254	1	US-08-774-592-3	Sequence 3, Appl
22	1305.5	49.6	247	3	US-08-944-483-49	Sequence 49, Appl
23	1289	48.9	241	1	US-08-330-978-4	Sequence 4, Appl
24	1289	48.9	241	1	US-08-474-042-4	Sequence 4, Appl
25	1289	48.9	241	1	US-08-484-558-4	Sequence 4, Appl
26	1289	48.9	241	1	US-08-774-592-4	Sequence 4, Appl
27	1051.5	39.9	461	6	5521070-2	Patent No. 5521070

QY 604 CCATATGATGACGCGACTGGACCCACCGAGAACCCCTTCGACCTGCTTGAAC 663  
Db 192 ----- 192  
QY 664 CAGACGACCTGAGAGGGCGACACAACTCACCAGGATCGTGGAGGCCAGGATGC 723  
Db 193 -----ArgilleValGlyGlyAsnValCys 200  
QY 724 AAGGACGGGAGTGTCCCTGCGAGGCCCTGCTC---ATCAATGAGGAAACGAGGGT--- 777  
Db 201 ProLysGlyGluCysProTirpGlnAlaValLeuLysIleAsn-----GlyLeu 216  
QY 778 ----TTCCTGTGGTGAACATTCTGAGCGAGTTCACATCTAACGGAGCCACTGTCTC 834  
Db 217 LeuLeuCysGlyAlaValLeuLeuAspAlaArgTirpIleValThrAlaAlaHisCysPhe 236  
QY 835 TACCAAGCCAAG-----AGATTCAAGGTAGGGTAGGGACCGCGAACCAGGAGCAG 885  
Db 237 AspAsnIleArgTyrTirpGlyAsnIleThrValValMetGlyGluHisAspPheSerGlu 256  
QY 886 GAGGAGCGGTGAGCGGTGCACGAGGTGGAGGTGTCTCATCAAGCACAAACCGGTTCACA 945  
Db 257 LysAspGlyAspGluGlnValArgValThrGlnValIleMetProAspLysTyrIle 276  
QY 946 AAGGAGACCTATGACTTCGACATCGCGTGTCTCGGCTCAAGACCCCATCCTCCGC 1005  
Db 277 ArgGlyLysIleAsnHisAspIleAlaLeuLeuArgLeuHisArgProValThrPheThr 296  
QY 1006 ATGAACGTGGCGCTGCTGCTCCCGAGGTGACTGGCGCGAGTCCACGCTCATGACG 1065  
Db 297 AspTyrValValProLeuCysLeuProGluLysSerPheSerGluAsnThrLeuAlaArg 316  
QY 1066 CAGAAGCGGGATTGTGAGCGGTTCGGCGCCACCCACAGAGAGGGCCGCGACGCCACC 1125  
Db 317 IleArgPheSerArgValSerGlyTirpGlyGlnLeuLeuAspArgGlyAlaThrAlaLeu 336  
QY 1126 AGGCTCAAAGATGCTGAGGTGCTTACGTGGACCGCACACCTGC----- 1170  
Db 337 GluLeuMetSerIleGluValProArgLeuMetThrGlnAspCysLeuGluHisAlaLys 356  
QY 1171 AAGCTGTCCAGACGCTTCATCATCACCAGAACATGTTCTGTGCGCGCTACGACACCAAG 1230  
Db 357 HisSerSerAsnThrProLysIleThrGluAsnMetPheCysAlaGlyTyrMetAspGly 376  
QY 1231 CAGGAGGATGCTGCCAGGGGAGAGCGGGGGCGCGACGTACCCGCTTCAAGGACACC 1290  
Db 377 ThrLysAspAlaCysLysGlyAspSerGlyGlyProHisAlaThrHisTyrHisGlyThr 396  
QY 1291 TACTTCGTGACAGGATCGTCAAGTGGGAGAGAGTGTGCGCGTAAAGGGGAAGTACGGG 1350  
Db 397 TirpTyrLeuThrGlyValValSerTirpGlyGlyCysAlaAlaIleGlyHisIleGly 416  
QY 1351 ATCTACACCAAGGTACCGCTTCTCAAGTGGATCGACAGGTCCATGAAACCAAGG 1407  
Db 417 ValTyrThrArgValSerGlnTyrIleAspTirpLeuValArgHisMetAspSerLys 435

Search completed: August 11, 2003, 10:48:03  
Job time 177.5 secs





























QY	018	CTGTGCTGCTCCCCGAGCGTGACTGGCGCGAGTCCACGCTGATGAGCGCAGAGACGCGG	1077
Db	337	ProAlaCysLeuProGlnLysAspTrpAlaGluSerThrLeuMetThrGlnLysThrGly	356
QY	078	ATTGTGAGCGCTTCGGCGCCACCCACGAGAGAGGGCGGCGAGTCCACCAGGCTCAAGATG	1137
Db	357	IleValSerGlyPheGlyArgThrHisGluGlyGlyArgGlnSerAsnIleLeuLysMet	376
QY	138	CTGAGGTGCCCTACGTGGACCCACACAGCTGCAAGCTGTCCAGCAGCTTCATCATCAACC	1197
Db	377	LeuGluValProTyrValAspArgAsnThrCysLysLeuSerThrSerPheSerIleThr	396
QY	198	CAGAACATGTTCTGTGCGCGCTACGACACCAACACGAGGAGGATCGCTGCCAGGGGACAGC	1257
Db	397	GlnAsnMetPheCysAlaGlyTyrGluAlaLysLeuGluAspAlaCysGlnGlyAspSer	416
QY	258	GGGGGCGCGACAGCTCACCCGCTCAAGGACACACCTACTTCGTGACAGGCATCGTCAGCTGG	1317
Db	417	GlyGlyProHisValThrArgPheLysAsnThrTyrTyrValThrGlyIleValSerTrp	436
QY	318	GGAGAGAGCTGTGCCCGTAAGGGGAGTAGTACGGGATCTACACCAAGGTCACCGCTTCCTC	1377
Db	437	GlyGluGlyCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrThrPheLeu	456
QY	378	AACTGGATCACAGGTCTCATGAAACACAGGCGTTCGCCAAGGCCAAGAGC	1428
Db	457	LysTrpIleaspArgSerMetLysAlaArgValGlyProThrAlaGluThr	473
RESULT 4			
Q63207	7	PRELIMINARY; PRT; 482 AA.	
ID	Q63207		
AC	Q63207		
DT	01-N-V-1996 (T-REMBLrel. 01, Created)		
DT	01-N-V-1996 (T-REMBLrel. 01, Last sequence update)		
DT	01-N-R-2003 (T-REMBLrel. 23, Last annotation update)		
DE	Factor X.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCBI TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAN-Sprague-Dawley;		
RC	MEDLINE=96093366; PubMed=8578539;		
RT	Staron C., Ross R.P., Hutson S., Wallin R.;		
RT	"Evidence for competition between vitamin K-dependent clotting factors		
RT	for intracellular processing by the vitamin K-dependent gamma-		
RT	carboxylase."		
RL	Third. Res. 80:63-73(1995).		
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
DR	EMBL X79807; CAA56202.1; -		
DR	HSSP P00742; IYKA.		
DR	MERCPS; S01.216; -		
DR	InterPro: IPR000152; Asx_hydroxyl.		
DR	InterPro: IPR001314; Chymotrypsin.		
DR	InterPro: IPR000742; EGF_2.		
DR	InterPro: IPR001881; EGF_CA.		
DR	InterPro: IPR001438; EGF-II.		
DR	InterPro: IPR006209; EGF-like.		
DR	InterPro: IPR002383; GLA_blood.		
DR	InterPro: IPR001254; Ser_protease_Try.		
DR	InterPro: IPR000294; VitK_dep_GLA.		
DR	Pfam PF00008; EGF; 2.		
DR	Pfam PF00594; gla; 1.		
DR	Pfam PF00089; trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	PRINTS; PR00010; EGFBL00D.		
DR	PRINTS; PR00001; GLABLO0D.		
DR	SMART; SM00179; EGF_CA; 1.		
DR	SMART; SM00069; GLA; 1.		
DR	SMART; SM00020; Tryp_Spc; 1.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.		

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Db 417 GlyGlyProHisValThrArgPheLysAsnThrTyrTyrValThrGlyIleValSerTtp 436
Qy 318 GGAGAGAGCTGCTCCCGTAAGGGAAGTACGGGATCTACACCAAGTCCACCGCTTCCTC 1377
Db 437 GlyGluGlyCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrPheLeu 456
Qy 378 AAGTGGATGACAGGTCATGAACACAGGGGCTTGCACAGGCCAAGAGC 1428
Db 457 LysTrpIleAspArgSerMetLysAlaArgValGlyProThrAlaGluThr 473

RESULT 3
O54740 PRELIMINARY; PRT; 481 AA.
ID OS4740
AC 054740
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR F410.
OS Mus musculus (Mouse).
OG Plasmodium bluescript.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98434993; PubMed=9783672;
RA Heidmann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998)
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL AJ222677; CAA10933.1; -
DR HSSR P00742; IYKA.
DR MEROPS; S01.216; -.
DR MGD MG1:103107; F10.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam PF00008; EGF; 2.
DR Pfam PF00594; gla; 1.
DR Pfam PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00003; GLABLO0D.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease; Signal;
KW Plasmod.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DE5EF9D7AE CRC64;

Alignment Scores:
Pred. No. 9,77e-138 Length: 481
Score: 1990.50 Matches: 364
Percent Similarity: 85.74% Conservative: 45

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Best Local Similarity: 76.31% Mismatches: 63
Query Match: 73.37% Indels: 5
DB: 11 Gaps: 2
US-09-632-722-1 (1-1467) x 054740 (1-481)

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DB 1 MetGlySerProValGlnLeuSerLeuLeuValValLeuAlaSerLeuLeuPro 20
QY 61 GGGAAAGTCTCTTCATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 21 GlyLysGlyValPheIleAsnArgGluAlaAsnValLeuAlaSerLeuArgArg 40
QY 121 GCGAATTCCTTCTTGAAGAGATGAAGAAAGACACCTCGAAAGAGAGTGCATGAGAG 180
DB 41 AlaAsnSerPhePheGluGluPheLysGlyAsnLeuGluArgGluCysMetGluGlu 60
QY 181 ACCTGCTCATAGAGAGGCGCGAGGAGTCTTTGAGGACACGACAGCAAGCAATTC 240
DB 61 IleCysSerTyrGluGluValArgGluIlePheGluAspAspGluLysThrLysGluTyr 80
QY 241 TGGATAATAACAAAGATGGCGACACAGTGTGAGACCACTCTGCCAGAACAGGCGAAA 300
DB 81 TrpThrLysTyrLysAspGlyAspGlnCysGluSerSerProCysGlnAsnGlnGlyAla 100
QY 301 TGTAAGAGCGGCTCGGGGAATACACCTGCACCTGTTTGAAGAGTTCGAAGGCAAAAC 360
DB 101 CysArgAspGlyIleGlyGlyTyrThrCysThrCysSerGluGlyPheGluGlyAsn 120
QY 361 TGTGAATTTATCACACGGAAGCTGTGACGCTGGACACACGAGGAGTGTGACCACTTC 420
DB 121 CysGluLeuPheValArgLysLeuCysArgLeuAspAsnGlyAspCysAspGlnPheCys 140
QY 421 CACGAGGAGCAACTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 141 ArgGluGluGlnAsnSerValValCysSerCysAlaSerGlyTyrPheLeuGlyAsnAsp 160
QY 481 GCGAAGGCTGCTATCCACACAGGCGCTTACCCCTGTGGGAAACACAGACCTGGAACG 540
DB 161 GlyLysSerCysIleSerThrAlaProPheProCysGlyLysIleThrThrGlyArgArg 180
QY 541 AAGAGTCTAGTGGCGCCAGCCACACAGCAGCAGCGGGG---GAGGCGCTCTGACAGTACA 597
DB 181 LysArgSerValAlaLeuAsnThrSerAspSerGluLeuAspLeuGluAspAlaLeu--- 199
QY 598 TGGAAAGCCATATGATGACCGCGCTGACCCCGAGAACCCCTTCGACCTCTGCTGAC 657
DB 200 -----LeuAspGluAspPheLeuSerProThrGluAsnProIleGluLeuLeuAsn 216
QY 658 TTCAACACAGCAGCCTGTGAGAGGGGCGGACAAACACCTCACAGGATCGTGGGAGCCAG 717
DB 217 LeuAsnGluThrGlnProGluArgSerSerAspLeuValArgIleValGlyArg 236
QY 718 GAATGCAAGGAGCGGGAGTGTCCCTGGCAGGCGCTGTCTCATCATGAGGAAACAGGGT 777
DB 237 GluCysLysAspGlyGluCysProTrpGlnAlaLeuLeuIleAsnGluAspAsnGluGly 256
QY 778 TTCTGTGTGGAACCTATTCTGAGCGAGTCTTACATCTCTAACCGCAGCCCTGCTCTAC 837
DB 257 PheCysGlyGlyThrIleLeuAsnGluPheTyrIleLeuThrAlaAlaHisCysLeuHis 276
QY 838 CAAGCCAAAGATTCAAGGTGAGGTGAGGAGCGGACCGGACCGGAGGAGGAGGCGGT 897
DB 277 GlnAlaArgArgPheLysValArgValGlyAspArgAsnThrGluLysGluAspGlyAsn 296
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QY 958 GACTTCGACATCGCGCTCGGCTCAAGAGCCCGCTCACCTTCCGCATCAAGTGGCG 1017
DB 317 AspTyrAspIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAla 336

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 11, 2003, 10:36:30 ; Search time 153.5 Seconds

(without alignments)  
4932.419 Million cell updates/sec

Title: US-09-632-722-1

Perfect score: 2713

Sequence: 1 atggggcgccaccgacct.....cgctctctccattaaagtga 1467

Scoring table:

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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database

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8: sp\_organelle:.\*  
9: sp\_phase:.\*  
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15: sp\_virus:.\*  
16: sp\_bacteriap:.\*  
17: sp\_archaeap:.\*

Pres. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	1093.5	73.5	481	11	O88947	O88947 mus musculu

2	1992.5	73.4	481	11	O99132	O99132 mus musculu
3	1990.5	73.4	481	11	O54740	O54740 mus musculu
4	1957	72.1	482	11	O63207	O63207 rattus norv
5	1706.5	62.9	469	6	O9GMD9	O9GMD9 ornithorhyn
6	1118	41.2	474	13	O8JHC8	O8JHC8 brachydanio
7	1114.5	41.1	376	13	P83370	P83370 hoplocephal
8	1039.5	38.3	456	4	Q14316	Q14316 homo sapien
9	1038.5	38.3	461	6	O95ND7	O95ND7 pan troglod
10	1003.5	37.0	461	6	O95ND6	O95ND6 pan troglod
11	946	34.9	701	4	O96PO8	O96PO8 homo sapien
12	936.5	34.5	433	13	O90VK1	O90VK1 brachydanio
13	935.5	34.5	433	13	O8JHD0	O8JHD0 brachydanio
14	932	34.4	503	13	O8AYE4	O8AYE4 brachydanio
15	909.5	33.5	446	11	O61109	O61109 mus musculu
16	904.5	33.3	446	11	O8K3U6	O8K3U6 rattus norv
17	862	31.8	456	6	O9TTR0	O9TTR0 canis famil
18	860.5	31.7	460	11	O91WN8	O91WN8 mus musculu
19	856.5	31.6	460	11	O99PC6	O99PC6 mus musculu
20	840	31.0	443	13	O8JHC9	O8JHC9 brachydanio
21	837	30.9	161	6	O28511	O28511 macaca mula
22	762	28.2	161	11	O60546	O60546 mesocricetu
23	762	28.1	161	11	O63109	O63109 rattus norv
24	724	26.7	159	6	O77669	O77669 canis famil
25	636	23.4	608	13	O9PTW7	O9PTW7 struthio ca
26	622	22.9	607	13	O91001	O91001 gallus gall
27	599	22.1	399	11	O9CQW3	O9CQW3 mus musculu
28	473.5	17.5	241	11	O8CI01	O8CI01 mus musculu
29	459	16.9	467	5	O967X8	O967X8 panulirus a
30	443	16.3	420	13	O90504	O90504 eptaretus
31	436	16.1	235	13	O91004	O91004 gekko gekko
32	435	16.0	767	13	O9DGR2	O9DGR2 xenopus lae
33	431.5	15.9	799	11	O9DBI0	O9DBI0 mus musculu
34	429.5	15.8	581	5	O81925	O81925 hyphantria
35	429.5	15.8	1524	13	O91674	O91674 xenopus lae
36	429	15.8	559	11	O91VP2	O91VP2 mus musculu
37	428.5	15.8	683	5	O8MRH5	O8MRH5 drosophila
38	428.5	15.8	787	5	QSVRE6	QSVRE6 drosophila
39	427	15.7	449	5	Q9VDU8	Q9VDU8 drosophila
40	425.5	15.7	247	11	O9CNP7	O9CNP7 mus musculu
41	423.5	15.6	560	4	Q14520	Q14520 homo sapien
42	421	15.5	802	4	O81UE2	O81UE2 homo sapien
43	421	15.5	811	4	O81U80	O81U80 homo sapien
44	420	15.5	390	5	O81927	O81927 hyphantria
45	417.5	15.4	138	6	Q28994	Q28994 sus scrofa

## ALIGNMENTS

RESULT 1

O88947	O88947	PRELIMINARY;	PRT;	481 AA.
AC	O88947;			
DT	01-NOV-1998 (TREMBlrel. 08, Created)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)			
DE	Coagulation factor X precursor.			
GN	F10.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL6 X CBA; TISSUE=Liver;			
RC	MEDLINE=98347933; PubMed=9684791;			
RA	Liang Z., Cooper A., Deford M.E., Carmeliet P., Collen D.,			
RA	Castellino F.J., Rosen E.D.;			
RT	"Cloning and characterization of a cDNA encoding murine coagulation			
RT	factor X.;"			
RL	Thromb. Haemost. 80:87-91(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129SJ;			





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EMBL	X64336;	CAA45617.1;	-		
DR	PIR;	SI8994;	SI8994.		
DR	HSSE	P04070;	1PCU.		
DR	MERC	S;	S01_218;		
DR	Inte	Pro;	IPR000152;	Asx_hydroxyl.	
DR	DR	Inte	Pro;	IPR001314;	Chymotrypsin.
DR	DR	Inte	Pro;	IPR001881;	EGF_CA.
DR	DR	Inte	Pro;	IPR006209;	EGF_like.
DR	DR	Inte	Pro;	IPR002383;	GLA_blood.
DR	DR	Inte	Pro;	IPR001254;	Ser.protease_Try.
DR	DR	Inte	Pro;	IPR000294;	VitK_dep_GLA.
DR	Pfam	PF00008;	EGF; 2.		
DR	Pfam	PF00594;	gla; 1.		
DR	Pfam	PF00089;	trypsin; 1.		
DR	PRIN	S;	PRO0722;	CHYMOTRYPSIN.	
DR	PRIN	S;	PRO0001;	GLABLOOD.	
DR	SMAP	; SM00179;	EGF_CA; 1.		
DR	SMAP	; SM00069;	GLA; 1.		
DR	SMAP	; SM00020;	Tryp_Spc; 1.		
DR	PRO	TE;	PS00010;	ASX_HYDROXYL; 1.	
DR	PRO	TE;	PS00022;	EGF_1; 1.	
DR	PRO	TE;	PS01186;	EGF_2; 2.	
DR	PRO	TE;	PS01187;	EGF_CA; 1.	
DR	PRO	TE;	PS00011;	GLU_CARBOXYLATION; 1.	
DR	PRO	TE;	FS00240;	TRYPsin_DOM; 1.	
DR	PRO	TE;	PS00134;	TRYPsin_HIS; 1.	
DR	PRO	TE;	PS00135;	TRYPsin_SER; 1.	
DR	Blood	coagulation;	Glycoprotein;	Serine protease;	
DR	Gamma	-carboxylglutamic acid;	Calcium-binding;	Vitamin K; Hydroxylation;	
KW	EGF	-like domain;	Repeat;	Endothelial cell; Hydrolase; Signal.	
FT	SIGN	L	1	32	BY SIMILARITY.
FT	PRO	PEP	33	41	BY SIMILARITY.
FT	CHAI	N	42	196	PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT	CHAI	N	199	461	PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT	PEPT	IDE	199	212	ACTIVATION PEPTIDE (BY SIMILARITY).
FT	SITE		212	213	CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT	DOM	A	N	96	EGF-LIKE 1.
FT	DOM	A	N	135	EGF-LIKE 2.
FT	DOM	A	N	213	SERINE PROTEASE.
FT	MOD	_ES	47	47	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD	_ES	48	48	(BY SIMILARITY).
FT	MOD	_ES	55	55	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD	_ES	57	57	(BY SIMILARITY).
FT	MOD	_ES	60	60	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD	_ES	61	61	(BY SIMILARITY).
FT	MOD	_ES	66	66	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD	_ES	67	67	(BY SIMILARITY).
FT	MOD	_ES	70	70	GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD	_ES	112	112	(BY SIMILARITY).
FT	MOD	_ES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT	_ITE	254	254	CHARGE RELAY SYSTEM.
FT	ACT	_ITE	300	300	CHARGE RELAY SYSTEM.
FT	ACT	_ITE	402	402	CHARGE RELAY SYSTEM.
FT	DISC	_FID	58	63	BY SIMILARITY.
FT	DISC	_FID	91	110	BY SIMILARITY.
FT	DISC	_FID	100	105	BY SIMILARITY.
FT	DISC	_FID	104	119	BY SIMILARITY.
FT	DISC	_FID	121	130	BY SIMILARITY.
FT	DISC	_FID	139	150	BY SIMILARITY.

FT	DISULFID	146	159	BY SIMILARITY.	
FT	DISULFID	161	174	BY SIMILARITY.	
FT	DISULFID	182	320	INTERCHAIN (BY SIMILARITY).	
FT	DISULFID	239	255	BY SIMILARITY.	
FT	DISULFID	373	387	BY SIMILARITY.	
FT	DISULFID	398	426	BY SIMILARITY.	
FT	CARBOHYD	215	215	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	291	291	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE	461 AA;	51912 MW;	8A4CF93664EDACD5 CRC64;	

Alignment Scores:		2,44e-44	Length:	461
Pred. No.:	Score:	861.00	Matches:	182
Best Local Similarity:	Percent Similarity:	52.60%	Conservative:	81
Query Match:	Best Local Similarity:	36.40%	Mismatches:	159
	Query Match:	31.74%	Indels:	78
DB:		1	Gaps:	11

US-09-632-722-1 (1-1467) x PRTC_RAT (1-461)	
QY	19 CTCGCTCCTCAGTGCCCTC-----CTGGCTGGCTCCTGCTGCTCGGGGAAAGT 69
Db	6 lIePheLeuLeuPheAlaSerThrTrpGlyIleSerGlyValSerAlaHisProAspPro 25
QY	70 CTGTTTCATCGGAGGAGCGCCACACATCCTCGCGAGGTGCAGGGGCAATTCC 129
Db	26 ValPheSerSerSerGluGlyAlaHisGlnValLeu---ArgValIleArgAlaAsnSer 44
QY	130 TTTCTTGAAGATGAAGAAAGGACACCTCGAAGAGATGTCATGGAAGAGACCTGCTCA 189
Db	45 PheLeuGluGluValArgAlaGlySerLeuGluArgGluCysMetGluGluIleCysAsp 64
QY	190 TAGCAAGAGCCCGGAGGTCTTTGAGGACAGCGCACAGCGAATGAATCTCGAATAAA 249
Db	65 PheGluGluAlaGlnGluIlePheGlnAsnValGluAspThrLeuAlaPheTrpIleLys 84
QY	250 TACAAGATGGCCACAGTGTGAGAC-----AGTCCTTCG 285
Db	85 TyrPheAspGlyAspGlnCysSerThrProLeuAspHisGlnCysAspSerProCys 104
QY	286 CAGAAGCAGGCGAAATGTAAAGAGCGGCTCGGGGAATACACTGCACCTGTTAGAGGA 345
Db	105 CysGlyHisGlyThrCysIleAspGlyLeuGlyGlyPheSerCysCysAspLysGly 124
QY	346 TTCAGAGGCAAAACTCTGTAATTATTACACAGGAAGCTC-----TGCAGCGCTG 393
Db	125 TrpGluGlyArgPheCysGln-----GlnGluMetGlyPheGlnAspCysArgVal 141
QY	394 GACAAGCGGACCTGTACCACTGTCTGCACAGGAACAGAACTCTGTGGTGTGCTCTGC 453
Db	142 LysAsnGlyGlyCysTyrHisTyrCysLeuGluGluThrArgGlyArgAIGCysArgCys 161
QY	454 GCCCGGGGTACACCTGGCTGCACACGGCAAGCGCTGCATTCACACGGCCCTACCCC 513
Db	162 AlaProGlyTyrGluLeuAlaAspAspHisMetHisCysArgProThrValAsnPhePro 181
QY	514 TGTGGGAAACACACCCTGGAGACGAGAAAGGTCTAGTGGCCCGACCCAGCAGCAGC 573
Db	182 CysGlyLys----- 184
QY	574 GGGGAGGCCCTTGACAGCATCACATGGAAGCCATATGAT-----GCA 615
Db	185 -----LeuTrpIleArgThrAspLysLysArgLysAsnPhelys 197
QY	616 GCGACCTGGACCCACCGAAGACCCCTTGACCTGCTTCACTTCAACCGACGACGCT 675
Db	198 ArgAspIleAspProGluAspGluGluLeu----- 209
QY	676 GAGAGGGCGACAAACACCTCACCATGATCGTGGGAGCCAGGAATGCAAGGACGGGAG 735
Db	210 -----GlyProArgIleValAsnGlyThrLeuThrLysGlnGlyAsp 223

Query Match:	32.14%	Indels:	52
DB:	1	Gaps:	10
US-09-632722-1 (1-1467) x PRTC_BOVIN (1-456)			
QY	64	GAAGAGTCTGTTTCATCCGAGGAGCAGCCCAACAACATCTCTGGCGAGGGTCCACGAGGCC	123
DB	21	AspSerValPheSerSerGlnArgAlaHisGlnValLeuLeuArgLysArgAla	40
QY	124	AATTCCTTTCTTGAAGAGATGAAGAAAGGACACCTCGAAAGAGAGTGCATGGGAAGACCC	183
DB	41	AsnSerPheLeuGluLeuArgProGlyAsnValGluArgGluCysSerGluGluVal	60
QY	184	TGCTCATACGAAGAGGCCCGAGGCTTTTGAGGACAGCACAAGCAATGATTCG	243
DB	61	CysGluPheGluGluAlaArgGluPheGlnAsnThrGluAspThrMetAlaPheT	80
QY	244	AATAAATCAAAAGATGCGACCGACCTGTGACACCACT	279
DB	81	SerPheTyrSerArgLysGlnCysGluAspArgProSerGlySerProCysAspLeu	100
QY	280	CCTTGGCCAGAACCGGCAATGTAAAGACGGCTCGGGAATACACCTGCACCTGTTTA	339
DB	101	ProCysCysGlyArgGlyLysCysIleAspGlyLeuGlyGlyPheArgCysAspCysAla	120
QY	340	GAAGGATTCGAAGCAAAACTGTGAATTATTCACAGC	396
DB	121	GluGlyTrpGluGlyArgPheCysLeuHisGluValArgPheSerAsnCysSerAlaGlu	140
QY	397	AACGGGACGTGTACCACTTCTCCAGCAGGAAGACAACCTCTGTGTGTCTCTCTGGCC	456
DB	141	AsnGlyCysAlaHisTyrCysMetGluGluGluGlyArgHisCysSerCysAla	160
QY	457	CGCGGTGTACCTGGCTGTCAACAGCGACCGCTGCATTCCTCCAGGGCCCTACCCCTGT	516
DB	161	ProGlyTyrArgLeuGluAspAspHisGlnLeuCysValSerLysValThrPheProCys	180
QY	517	GGGAAA-----CAGACCCCTGGACCGCAGGAAGGTGCTGGCCAGGCCACCCAGCAGC	570
DB	181	GlyArgLeuGlyLysArgMetGluLysLysArgLysThrLeuLysArgAspThrAsnGln	200
QY	571	AGCGGGAGGCCCTTGACACATCATATGATGAGCCATATATGTCAGCCGAC	627
DB	201	-----ValAspGlnLysAspGlnLeuAsp	208
QY	628	CCACCGAGAACCCCTTCGACCTGTGACTTCAACAGCAGCGCCTGAGAGGGGGCAG	687
DB	209	Pro-----	209
QY	688	AACAACCTACCGAGTCTGGGAGCGCAGGAATGCAAGACGGGAGTGCCTCCGCGAG	747
DB	210	-----ArgIleValAspGlyGlnGluAlaGlyTrpGlyGluSerProT	225
QY	748	GCCTCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACTATCTTGTGACGAGTTC	807
DB	226	AlaValLeuLeuAspSerLysLysLeuValCysGlyAlaValLeuIleHisValSer	245
QY	808	TACATCCTAACGCGACCCACTCTCTCTACCAAGCCCAAGAGATCAAGGTGAGGGTAGGG	867
DB	246	TrpValLeuThrValAlaHisCysLeuAspSerArgLysLysLeuIleValArgLeuGly	265
QY	868	GACCGGAACACGAGGAGGAGGGCGGTGAGCGGTGCACGAGGTGAGGTGTCATC	927
DB	266	GluTyrAspMetArgTrpGluSerTrpGluValAspLeuAspIleLysGluValIle	285
QY	928	AGACACAACCGGTTCACAAGGAGACCTATGACTTCGACATCCCGCTGTCTCCGGCTCAAG	987
DB	286	IleHisProAsnTyrThrLysSerThrSerAspAsnAlaLeuLeuArgLeuAla	305
QY	988	ACCCCCATCACCTTCGCATGAACGTGGCGCCCTGCTCCCTCCCGAGCGTGA	1047
DB	306	LysProAlaThrLeuSerGlnThrIleValProIleCysLeuProAspSerGlyLeuSer	325

Qy	1048	GAGTCC-----ACGCTGATGACGACGAAGACGGGGATTGTGTAGCGCGCTTCGGGCGCAC	1101
Db	326	GLuArgLysLeuThrGlnValGlyGlnGluThr---ValValThrGlyTrpGlyTyrArg	344
Qy	1102	CACGAAGAAGCGCGCGAGTCACCC--AGCCTCAAGATGCTGGAGGTGCCCTACGTGGAC	1158
Db	345	AspGluThrLysArgAsnArgThrPheValLeuSerPheIleLysValProValValPro	364
Qy	1159	CGCAACAGCTGCGAAGCTGTCCACAGCAGTCATCACCACGACAACTGTCTGTGTGGCGG	1218
Db	365	TyrAsnAlaCysValHisAlaMetGluAsnLysIleSerGluAsnMetLeuCysAlaGly	384
Qy	1219	TACCACACCAGCAGGAGGTGCTGCCAGGCGGACAGGGGGCCCGACGTCACCCCG	1278
Db	385	IleLeuGlyAspProArgAsnPalCysGluGlyAspSerGlyGlyProMetValThrPhe	404
Qy	1279	TTCAAAGACACCTACTCTGTGACAGGCATCGTCAGCTGGGGAGAGAGCTGTGCCGTAAG	1338
Db	405	PheArgGlyThrTrpPheLeuValGlyLeuValSerTrpGlyGluGlyCysGlyArgLeu	424
Qy	1339	GGGAAGTACGGGATCTACCAAGAGTCACCGCCTTCCTCAAGTGGATCGACAGTCCATG	1398
Db	425	TyrAsnTyrGlyValTyrThrLysValSerArgTyrLeuAspTrpIleTyrGlyHisIle	444
Qy	1399	AAAACCAAGGGCTTGCCCAAGGCGCAAGCCATGCCCGC	1437
Db	445	LysAlaGlnGluAlaPro---LeuGluSerGlnValPro	456
		RESULT 15	
		ID PRTC_RAT STANDARD; PRT; 461 AA.	
AC	P31394;		
DT	01-JUL-1993 (Rel. 26, Created)		
DT	01-JUL-1993 (Rel. 26, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Vitamin K-dependent protein C precursor (EC 3.4.21.69)		
DE	(Autoproteolytic IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).		
Qy	GN PROC.		
Qy	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCBI_TaxID=10116;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Wistar; TISSUE=Liver;		
RX	MEDLINE=92329550; PubMed=1627650;		
RA	Okafuji T., Maekawa K., Nawa K., Marumoto Y.;		
RT	"the cDNA cloning and mRNA expression of rat protein C.";		
RL	Biochem. Biophys. Acta 1131:329-332(1992).		
CC	-  FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT		
CC	REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA		
CC	IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.		
CC	-  CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va		
CC	and VIIIA.		
CC	-  SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED		
CC	INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE		
CC	BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A		
CC	TETRADECAPTEIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS		
CC	REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS		
CC	STRONGLY PROMOTED BY THROMBOMODULIN.		
CC	-  TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.		
CC	-  PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME		
CC	GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.		
CC	-  MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO		
CC	ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING		
CC	SITE IS NECESSARY FOR THE RECOGNITION OF THE		
CC	THROMBIN-THROMBOMODULIN COMPLEX.		
CC	-  SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
CC	-  SIMILARITY: Contains 2 EGF-like domains.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation.		
CC	-----		

RA Long G.L., Balagaje R.M., McGillivray R.T.A.;  
RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";  
RL Proc Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
RN [2]  
RA SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.  
RX MEDLINE=83007325; PubMed=6896876;  
RA Fernlund P., Stenflo J.;  
RT "Amino acid sequence of the light chain of bovine protein C.";  
RL J. Biol. Chem. 257:12170-12179(1982).  
RN [3]  
RA REVISION TO 110.  
RX MEDLINE=83169769; PubMed=6572939;  
RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;  
RT "beta-hydroxyaspartic acid in vitamin K-dependent protein C.";  
RL Proc Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
RN [4]  
RA SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350  
RX AND ASN-366.  
RA MEDLINE=83007326; PubMed=6896877;  
RA Stenflo J., Fernlund P.;  
RT "Amino acid sequence of the heavy chain of bovine protein C.";  
RL J. Biol. Chem. 257:12180-12190(1982).  
RN [5]  
RA PROCESSING, AND CALCIUM-BINDING DATA.  
RX MEDLINE=83213513; PubMed=6304092;  
RA Esmon N.L., DeBault L.E., Esmon C.T.;  
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-  
domainless protein C";  
RL J. Biol. Chem. 258:5548-5553(1983).  
RN [6]  
RA PROCESSING, AND CALCIUM-BINDING DATA.  
RX MEDLINE=83213514; PubMed=6406503;  
RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;  
RT "Structural changes required for activation of protein C are induced  
by Ca2+ binding to a high affinity site that does not contain gamma-  
carboxyglutamic acid.";  
RL J. Biol. Chem. 258:5554-5560(1983).  
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
and VIIIA.  
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS  
REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
STRONGLY PROMOTED BY THROMBOMODULIN.  
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
SITE IS NECESSARY FOR THE RECOGNITION OF THE  
THROMBIN-THROMBOMODULIN COMPLEX.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: Contains 2 EGF-like domains.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
-----  
CC EMBL K02435; AAA30685.1; -;  
DR PTR# A26250; KXBO.  
DR HSS# P04070; LPCU.  
DR MER# S; S01.218; -;  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR001881; EGF\_Ca.

DR InterPro: IPR006209; EGF\_like.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR006210; IEGF.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF; 2.  
DR Pfam: PF00594; gla; 1.  
DR Pfam: PF00089; trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00181; EGF; 2.  
DR SMART: SM00069; GLA; 1.  
DR SMART: SM00020; Tryp\_SPC; 1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_CA; 1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Blood coagulation; Glycoprotein; Serine protease;  
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
FT NON\_TER 1  
FT SIGNAL <1 29  
FT PROPEP 30 39  
FT CHAIN 40 194  
FT CHAIN 197 456  
FT PEPTIDE 197 210  
FT DOMAIN 94 129  
FT DOMAIN 133 173  
FT DOMAIN 211 456  
FT MOD\_RES 45 45  
FT MOD\_RES 46 46  
FT MOD\_RES 53 53  
FT MOD\_RES 55 55  
FT MOD\_RES 58 58  
FT MOD\_RES 59 59  
FT MOD\_RES 62 62  
FT MOD\_RES 64 64  
FT MOD\_RES 65 65  
FT MOD\_RES 68 68  
FT MOD\_RES 74 74  
FT MOD\_RES 110 110  
FT ACT\_SITE 252 252  
FT ACT\_SITE 298 298  
FT ACT\_SITE 397 397  
FT DISULFID 56 61  
FT DISULFID 89 108  
FT DISULFID 98 103  
FT DISULFID 102 117  
FT DISULFID 119 128  
FT DISULFID 137 148  
FT DISULFID 144 157  
FT DISULFID 159 172  
FT DISULFID 180 318  
FT DISULFID 237 253  
FT DISULFID 368 382  
FT DISULFID 393 421  
FT CARBOHYD 136 136  
FT CARBOHYD 289 289  
FT CARBOHYD 350 350  
FT CARBOHYD 366 366  
FT VARIANT 82 82  
FT CONFLICT 455 456  
SQ SEQUENCE 456 AA; 51407 MW; CAAF6833F894C209 CRC64;  
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Alignment Scores:  
Pred. No.: 5.35e-45 Length: 456  
Score: 872.00 Matches: 183  
Percent Similarity: 56.24% Conservative: 83  
Best Local Similarity: 38.69% Mismatches: 155  
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N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
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N-LINKED (GLCNAC. . .).  
F -> K.  
VP -> PV (IN REF. 4).  
CAAF6833F894C209 CRC64;

FT DISULFID 55 70 BY SIMILARITY.  
 FT DISULFID 72 81 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
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 FT DISULFID 159 164 BY SIMILARITY.  
 FT DISULFID 178 194 BY SIMILARITY.  
 FT DISULFID 310 329 BY SIMILARITY.  
 FT DISULFID 340 368 BY SIMILARITY.  
 FT MOD\_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 52 52 O-LINKED (GLC. . .).  
 FT CARE\_DHYD 145 145 N-LINKED (GLCNAC. . .).  
 FT CARE\_DHYD 203 203 N-LINKED (GLCNAC. . .).  
 SQ SEQUENCE 407 AA; 44431 MW; 703E1FE06367F10 CRC64;

## Alignment Scores:

Pred. No. 5,27e-45 Length: 407  
 Score: 872.00 Matches: 174  
 Percent Similarity: 54.44% Conservativity: 71  
 Best Local Similarity: 38.67% Mismatches: 137  
 Query Match: 32.14% Indels: 68  
 DB: 1 Gaps: 9

US-09-632-722-1 (1-1467) x FA7\_BOVIN (1-407)

QY 121 GCCAATTCCTTTCTTGAAGAGATGAAGAAGACACCTCGAAGAGAGAGTGCATGGAAGAG 180  
 DB 1 AlaAsnGlyPheLeuGluGluLeuLeuProGlySerLeuGluArgGluCysArgGluGlu 20  
 QY 181 ACCTGCTCATACGAAGAGCCCGGAGGCTCTTCAGACAGCAGCAGCAAGCAATGAATTC 240  
 DB 21 LeuCysSerPheGluGluAlaHisGluPheArgAsnGluGluArgThrArgGlnPhe 40  
 QY 241 TGAATAATAACAAGATGGCGACAGTGTGAGACCACTCTCCAGAACACCGGCGAAA 300  
 DB 41 TrpValSerTyrAsnAspGlyAspGlnCysAlaSerSerProCysGlnAsnGlyGlySer 60  
 QY 301 TGTAAGACGCCCTCGGGGAATACACCTGCACCTGTTTGAAGATTGGAAGGCAAAAC 360  
 DB 61 CysGluAspGlnLeuArgSerTyrIleCysPheCysProAspGlyPheGluGlyArgAsn 80  
 QY 361 TGTGAATTA-----TTCACACGGAAGCTCTGCAGCTGGACAGCGGGGACTGTGACCA 414  
 DB 81 CysGluThrAspLysGlnSerGlnLeuIleCysAlaAsnAspAsnGlyGlyCysGluGln 100  
 QY 415 TTCTGCCACGAGGAACAAGACTCT---GTGGTGTCTCTCGCCCGCGGGGTACACCCCTG 471  
 DB 101 TyrCysGlyAlaAspProGlyAlaGlyArgPheCysTrpCysHisGluGlyTyrAlaLeu 120  
 QY 472 GCTGACACGCGAGGCGCTGATTCACACAGGCGCCCTACCCCTGTGGGAAA---CAGACC 528  
 DB 121 GlnAlaAspGlyValSerCysAlaProThrValGluTyrProCysGlyLysIleProVal 140  
 QY 529 CTGGAACCGCAAGAGGTGCTGAGTGGCCCGCCACCCAGCAGCAGCGGGAGGCCCTGAC 588  
 DB 141 LeuGluLysArgAsnGlySerLysProGlnGly----- 151  
 QY 589 AGCATCATGGAAGCCATATGATGCAGCCGACCTGGACCCACCCAGAACCCCTTCGAC 648  
 DB 151 ----- 151  
 QY 649 CTGCTTGACTCAACACGACCGCCTGTGAGAGGGCGGCGACACAAACCTCACACGAGCGTG 708  
 DB ----- 708

DB 152 -----ArgIleVal 154  
 QY 709 GGAGGCCAGGAATGCAAGGACGGGAGTGTCTCCCTGGCAGGCGCTCTCATCATGAGGAA 768  
 DB 155 GlyGlyHisValCysProLysGlyGluCysProTrpGlnAlaMetLeu---LysLeuAsn 173  
 QY 769 AACGAGGGTTCTGTGGTGAACACTATTCTGAGCGAGTTCTACATCCTAACGACGCCAC 828  
 DB 174 GlyAlaLeuLeuCysGlyGlyThrLeuValGlyProAlaTrpValValSerAlaAlaHis 193  
 QY 829 TGTCTCTACCAAGCCCAAGAGATTCAAGTGAGG-----GTAGGGGAC 870  
 DB 194 CysPhe-----GluArgLeuArgSerArgGlyAsnLeuThrAlaValLeuGlyGlu 210  
 QY 871 CGGAACACGAGCAGGAGGAGGCGGTGAGCGGTGCACGAGGTGAGGTGTCATCAAG 930  
 DB 211 HisAspLeuSerArgValGluGlyProGluGlnGluArgArgValAlaGlnIleVal 230  
 QY 931 CACAACCGGTTCCAAAAGAGAGACCTATGACTTCGACATCGCGTCTCCGGTCAAGACC 990  
 DB 231 ProLysGlnTyr-ValProGlyGlnThrAspHisAspValAlaLeuLeuGlnLeuAlaGln 250  
 QY 991 CCCATCACCTTCGGATGAACGTGGCGCTGCTCCCGAGCGGTGACTGGGCCGAG 1050  
 DB 251 ProValAlaLeuGlyAspHisValAlaProLeuCysLeuProAspProAspPheAlaAsp 270  
 QY 1051 TCCACGCTGATGACGCGAAGAGCGGGATTGTGAGCGGCTTCGGCGCACCCACGAGAG 1110  
 DB 271 GlnThrLeuAlaPheValArgPheSerAlaValSerGlyTrpGlyGlnLeuGluArg 290  
 QY 1111 GGCGCGCATCCACAGGCTCAAGATGCTGGAGGTGCCCTACGTGGACCGCGCACAGCTGC 1170  
 DB 291 GlyValThrAlaArgLysLeuMetValValLeuValProArgLeuLeuThrGlnAspCys 310  
 QY 1171 AGCTGCTCAGC-----ACGTCATCATCACCACAGACATGTCGTGTGCC 1215  
 DB 311 LeuGlnGlnSerArgGlnArgProGlyGlyProValValThrAspAsnMetPheCysAla 330  
 QY 1216 GGCTACGACACCAAGCAGGAGGATGCTGCCAGGGGACAGCGGGGCGCGCACGTCACC 1275  
 DB 331 GlyTyrSerAspGlySerLysAspAlaCysLysGlyAspSerGlyGlyProHisAlaThr 350  
 QY 1276 CGCTTCAAGACACCTACTCTGTGACAGCATCTGTCAGTGGGGAGAGAGTGTGCCCT 1335  
 DB 351 ArgPheArgGlyThrTrpPheLeuThrGlyValValSerTrpGlyGlyCysAlaAla 370  
 QY 1336 AAGGGAAGTACGGGATCTACACCAAGTCCCGCTTCTCAAGTGGATGCACAGGTCC 1395  
 DB 371 AlaGlyHisPheGlyIleTyrThrArgValSerArgTyrThrAlaTrpLeuArgGlnLeu 390  
 QY 1396 ATGAAACACGAGGGCTTCGCCAAGGCAAG 1425  
 DB 391 Met-----GlyHisProProSerArg 397  
 RESULT 14  
 PRTC\_BOVIN  
 ID PRTC\_BOVIN STANDARD; PRT; 456 AA.  
 AC P00745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85014826; PubMed=6091100;

201 ProLysGlyCysProTrpGlnAlaValLeuLysIleAsn-----GlyLeu 216  
778 ---TTCTGTGGTGAAGTCTTCTGAGCGAGTCTACATCCTAACGGCAGCCACCTGTCTC 834  
217 LeuLeuGlyAlaValLeuLeuAspAlaArgTPrIleValThrAlaAlaHisCysPhe 236  
835 TACCAAGCCAAAG-----AGATTCAAGGTGAGGGTAGGGAGCGGGAACACGAGCAG 885  
237 AspAsnIleArgTyrTrpGlyAsnIleThrValValMetGlyGluHisAspSerGlu 256  
886 GAGGAGGCGGTGAGCGGTGACGAGGTGGAGGTGGTATCATCAACACACCGGTTCACA 945  
257 LysAspGlyAspGluGlnValArgValThrGlnValIleMetProAspLysTyrIle 276  
946 AAGGAGACCATATGATCTGCATCGCGGTCTCCGGCTCAACACCGCCATCACTCCGC 1005  
277 ArgGlyLysIleAsnHisAspIleAlaLeuLeuArgLeuHisArgProValThrPheThr 296  
1006 ATGAAGTGGCGCTGCTGCTCCCTCCCGAGCTGACTGGCGGAGTCCACGCTGATGAGC 1065  
297 AspTyrValValProLeuLysLeuProGluLysSerPheSerGluAsnThrLeuAlaArg 316  
1066 CAGAAGACGGGATTTGAGCGGCTTCGGCGCCACCCAGCAGAGCGGCGGAGTCCACC 1125  
317 IleArgPheSerArgValSerGlyTrpGlyGlnLeuLeuAspArgGlyAlaThrAlaLeu 336  
1126 AGGCTCAAGATGCTGAGGTGCGCTACGTGGGACCGACGAGTGC----- 1170  
337 GluLeuMetSerIleGluValProArgLeuMetThrGlnAspCysLeuGluHisAlaLys 356  
1171 AGCTGTCGAGCGTTCATCATCAACCCAGAGATGTTCTGTGCGCGGTGACACACCAAG 1230  
357 HisSerSerAsnThrProLysIleThrGluAsnMetPheCysAlaGlyTyrMetAspGly 376  
1231 CAGGAGGATGCTGCCAGGGGACAGCGGGGCGCGGCGGCGGCGGCGGCGGCGGCGG 1290  
377 ThrLysAspAlaCysLysAspSerGlyGlyProHisAlaThrHisTyrHisGlyThr 396  
1291 TACTTCTGTCAGAGGATGCTGAGTGGGAGAGAGTGTGCCCGTAAGGGAGTACGGG 1350  
397 TrpTyrLeuThrGlyValValSerTrpGlyGluGlyCysAlaAlaIleGlyHisIleGly 416  
1351 ANCTACACCAAGTCAACCGCTTCTCAAGTGGATGCGAGTCCATGCAAAACCAAGG 1407  
417 ValTyrArgValSerGlnTyrIleAspTrpLeuValArgHisMetAspSerLys 435

RESULT 13  
FA7 BOVIN STANDARD; PRT; 407 AA.  
AC P2247;  
DT 01-AG-1991 (Rel. 19, Created)  
DT 01-AG-1991 (Rel. 19, Last sequence update)  
DT 28-EB-2003 (Rel. 41, Last annotation update)  
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
GN F7.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OC NCBI TaxID=9913;  
RP SEQUENCE.  
RX MEDLINE=89008362; PubMed=3049594;  
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.;  
RT "Bovine factor VII. Its purification and complete amino acid sequence.";  
RL J. Biol. Chem. 263:14868-14877(1988).  
RN [2].  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=89213999; PubMed=3149637;  
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,

Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX.";  
RL J. Biochem. 104:867-868(1988).  
RN [3].  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";  
RL Adv. Exp. Med. Biol. 281:121-131(1990).  
CC -!- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
CC -!- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.  
CC -!- TISSUE SPECIFICITY: Plasma.  
CC -!- PH: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC PIR: A31979; KFB07.  
DR HSP: P08709; IBF9.  
DR MEROPS: S01.215; -.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ga.  
DR InterPro: IPR001438; EGF\_II.  
DR InterPro: IPR006209; EGF-like.  
DR InterPro: IPR002383; GLA-like.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF; 2.  
DR Pfam: PF00594; gla; 1.  
DR Pfam: PF00089; trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR PRINTS: PR00010; EGFBL00D.  
DR PRINTS: PR00001; GLABLOOD.  
DR SMART: SM00179; EGF\_CA; 1.  
DR SMART: SM00069; GLA; 1.  
DR SMART: SM00020; Tryp\_Spc; 1.  
DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_CA; 1.  
DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE: PS00240; TRYPsin\_DOM; 1.  
DR PROSITE: PS00134; TRYPsin\_HIS; 1.  
DR PROSITE: PS00135; TRYPsin\_SER; 1.  
KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat.  
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.  
FT CHAIN 153 407 FACTOR VII HEAVY CHAIN.  
FT DOMAIN 6 35 GLA-RICH.  
FT DOMAIN 46 82 EGF-LIKE 1. CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 87 128 EGF-LIKE 2.  
FT DOMAIN 153 407 SERINE PROTEASE.  
FT SITE 152 153 CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN).  
FT ACT SITE 193 BY SIMILARITY.  
FT ACT SITE 242 BY SIMILARITY.  
FT ACT SITE 344 BY SIMILARITY.  
FT BINDING 338 SUBSTRATE (BY SIMILARITY).  
FT DISULFID 17 22 BY SIMILARITY.  
FT DISULFID 50 61 BY SIMILARITY.







RT epidermal growth factor-like domain of human factors VII and IX and  
 RL protein z and bovine protein z.";  
 J. Biol. Chem. 264:20320-20325(1989).  
 [7]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE-91344709; PubMed-2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RL first EGF-like domain of clotting factors VII and IX and protein Z.";  
 Adv. Exp. Med. Biol. 281:121-131(1990).  
 [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE-96175641; PubMed-8598903;  
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RL VIIa with soluble tissue factor.";  
 Nature 380:41-46(1996).  
 [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE-99126538; PubMed-9925787;  
 RA Zhan E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RL inhibited with a BPTI mutant.";  
 J. Mol. Biol. 285:2089-2104(1999).  
 [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE-98367502; PubMed-9692950;  
 RA Murayama A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,  
 RA Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RL factor VII.";  
 Biochemistry 37:10605-10615(1998).  
 [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE-91300046; PubMed-20700047;  
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Meach T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RL molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 Blood 78:132-140(1991).  
 [12]  
 RP VARIANT GLN-364 AND PHE-370.  
 RX MEDLINE-92340074; PubMed-1634227;  
 RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Rodolfo G., Casonato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RL polymorphism in the factor VII gene (F7).";  
 Hum. Genet. 89:497-502(1992).  
 [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE-93372811; PubMed-8364544;  
 RA Marchetti G., Ferrati M., Patraccchini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms  
 RL (115His and 333Ser) in the human coagulation factor VII gene.";  
 Hum. Mol. Genet. 2:1055-1056(1993).  
 [14]  
 RP VARIANT.  
 RX MEDLINE-94061028; PubMed-8242057;  
 RA Takaiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,  
 RA von Felten A., Melli E., Hahn I., Prangnell D.R., Lumley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RL polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 Hum. Mol. Genet. 2:1355-1359(1993).  
 [15]  
 RP VARIANT.  
 RX MEDLINE-94264305; PubMed-8204879;  
 RA Chabig S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,  
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the

RT cleavage site for activation and altering binding to tissue factor.";  
 RL Blood 83:3524-3535(1994).  
 [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE-95072589; PubMed-7981691;  
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RL factors VII (29Ala-->Val) and X (334Ser-->Pro).";  
 Hum. Mol. Genet. 3:1175-1177(1994).  
 [17]  
 RP VARIANT MIE HIS-307.  
 RX MEDLINE-95064662; PubMed-7974346;  
 RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,  
 RA Suzuki K.;  
 RT "Factor VII MIE: homozygous asymptomatic type I deficiency caused by  
 RL an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain.";  
 Thromb. Haemost. 71:773-777(1994).  
 [18]  
 RP VARIANT MET-419.  
 RX MEDLINE-96247510; PubMed-8652821;  
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary  
 RL deficiency causes defective secretion of the molecule.";  
 Blood 87:5085-5094(1996).  
 [19]  
 RP VARIANT.  
 RX MEDLINE-97001216; PubMed-8844208;  
 RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RL deficiency.";  
 Hum. Mutat. 8:108-115(1996).  
 [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE-97037613; PubMed-8883260;  
 RA Tanary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,  
 RA Zaizov R., Seligsohn U.;  
 RT "Ala244Val is a common, probably ancient mutation causing factor VII  
 RL deficiency in Moroccan and Iranian Jews.";  
 Thromb. Haemost. 76:283-291(1996).  
 [21]  
 RP VARIANT MORIOKA PRO-13.  
 RX MEDLINE-98235713; PubMed-9576180;  
 RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,  
 RA Sakuragawa N.;  
 RT "Factor VII Morioka (FVII L-26P): a homozygous missense mutation in  
 RL the signal sequence identified in a patient with factor VII  
 RT deficiency.";  
 Br. J. Haematol. 101:47-49(1998).  
 [22]  
 RP VARIANT.  
 RX MEDLINE-98112461; PubMed-9452082;  
 RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RL factor VII gene.";  
 Hum. Mutat. Suppl. 1:S189-S191(1998).  
 [23]  
 RP VARIANT.  
 RX MEDLINE-99318093; PubMed-10391209;  
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RL of human genes.";  
 Nat. Genet. 22:231-238(1999).  
 Alignment Scores:  
 Pred. No.: 1 53e-49 Length: 466  
 Score: 948.00 Matches: 189





DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS00240; TRYPsin\_DOM; 1.  
 DR PROSITE; PS00134; TRYPsin\_HIS; 1.  
 DR PROSITE; PS00135; TRYPsin\_SER; 1.  
 KW Blood coagulation; Plasma; Serine protease; Calcium-binding;  
 KW Hydrolase; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid;  
 KW Hemophilic; Hydroxylation; Zymogen; BGF-like domain.  
 FT CHAIN 1 146  
 FT PROPEP 147 181  
 FT CHAIN 182 416  
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 FT SITE 181 182  
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 FT MOD\_RES 64 64  
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 FT DISULFID 51 62  
 FT DISULFID 56 71  
 FT DISULFID 73 82  
 FT DISULFID 88 99  
 FT DISULFID 95 109  
 FT DISULFID 111 124  
 FT CARBHYD 53 53  
 FT CARBHYD 158 158  
 FT CARBHYD 168 168  
 FT CARBHYD 173 173  
 FT CARBHYD 261 261  
 FT ACT\_SITE 222 222  
 FT ACT\_SITE 270 270  
 FT ACT\_SITE 366 366  
 FT VARIANT 64 64  
 SQ SEQUENCE 416 AA; 46785 MW; 34A7DFE916330662 CRC64;

Alignment Scores:  
 Pred. No. 1.92e-50 Length: 416  
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 133 CTTGAAGAGATGAAGAAGACACCTCGAAGAGAGTGATGAGAGACCTGCTCATAC 192  
 6 LeuGlulupheValargGlyAsnLeuGluArgGlyCysGlyGluGluLysCysSerPhe 25  
 193 GAAGAGCCCGCGAGGTCTTTGAGGACAGCGACAAGCAATGAATCTGGAATAATAC 252  
 26 GluGluAlaArgGluValPheGluAsnThrGluLysThrThrGluPheTrpLysGlnTyr 45  
 253 AAGATGGGACCAAGTGTGAGACCACTCTTCCAGAACACAGGCAATGTAAAGACGCC 312  
 46 ValAspGlyAspGlnCysGluSerAsnProCysLeuAsnGlyGlyMetCysLysAsp 65  
 313 CTCGGGGAATACACCTGCACCTGTTTAGAAGAGATTCGAAGGCAAAACCTGTAATTTC 372  
 66 IleAsnSerTyrGluCysTrpCysGlnAlaGlyPheGluGlyThrAsnCysGluLeu --- 84

QY 373 ACACGGAAGCTCTGCACCTGGACACACGGGGACTGTGACCAAGTTCTGC ---CACAGGAA 429  
 DB 85 ---AspAlaThrCysSerIleLysAsnGlyArgCysLysGlnPheCysLysArgAspThr 103  
 QY 430 CAGAACTCTGTGGTGTCTCTGCTGGCCGGGGGTACACCTGGCTGACACAGGCAAGGCC 489  
 DB 104 AspAsnLysValValCysSerCysThrAspGlyTyrArgLeuAlaGluAspGlnLysSer 123  
 QY 490 TGCATTCCACAGGCGCTACCTGCTGGGAAACAGACCTCTGGAACACGAGCAAGAGTCA 549  
 DB 124 CysGluProAlaValProPheProCysGlyArgValSerValSerHisIleSerLysLys 143  
 QY 550 GTGCCCCAGGCC ---ACCAGCAGCAGCGGGGAGGCCCTTCGACAGC 591  
 DB 144 LeuThrArgAlaGluThrIlePheSerAsnThrAsnTyrGluAsnSerSerGluAlaGlu 163  
 QY 592 ATCATATGGAACCATATGATGACCGACCTGTGACCCCGAGAGACCCCTTCGACCTG 651  
 DB 164 IleIleTrpAsp --- 167  
 QY 652 CTTCATTCACACAGCAGCAGCTGTGAGGGGGGACAAACACCTCACAGGATCGTGGGA 711  
 DB 168 ---AsnValThrGlnSerAsnGlnSerPheAspGluPheSerArgValValGly 184  
 QY 712 GCCAGGAATCAAGAGCGGGAGTGTCCCTGGCAGGCGCTGTCTCATCAATGAGGAAAC 771  
 DB 185 GlyGluAspAlaGluArgGlyGlnPheProTrpGlnValLeuLeu ---HisGlyGluLeu 203  
 QY 772 GAGGTTTCTGTGTGGNACTATTCTGAGCGAGTCTACATCTTAACGGCAGCCACTGT 831  
 DB 204 AlaAlaPheCysGlyGlySerIleValAsnGluLysTrpValValThrAlaAlaHisCys 223  
 QY 832 CTCTACCAAGCAAGAGATTCAGGTGAGGTAGGGACCGGAAACACAGCAGCAGGAGG 891  
 DB 224 IleLysProGlyValLysIleThrValValAlaGluGluHisAsnThrGluLysProGlu 243  
 QY 892 GCGGTGAGCGGTGCACAGGTGAGGTGTCTATCAAGCAACACCGGTCTCACAAG --- 948  
 DB 244 ProThrGluGlnLysArgAsnValIleArgAlaIleProTyrHisSerTyrAsnAlaSer 263  
 QY 949 ---GAGACCTATGATCTCGACATCGCTGTCCGCTCAAGACCCCATCACCTCCGCG 1005  
 DB 264 IleAsnLysTyrSerHisAspIleAlaLeuLeuGluLeuAspGluProLeuGluLeuAsn 283  
 QY 1006 ATGAACGTGGCGCTGCTGCTCCCGAGCGTGACTGGCGCGAGTCCACGCTGATGACG 1065  
 DB 284 SerTyrValThrProIleCysIleAlaAspArgAspTyr ---ThrAsnIlePhe 300  
 QY 1066 CAGAAG ---ACGGGATTTGTGAGCGGTCTCGGGCGCCACCCACAGAGAGGGCGGCGAG 1119  
 DB 301 SerLysPheGlyTyrGlyTyrValSerGlyTrpGlyLysValPheAsnArgGlyArgSer 320  
 QY 1120 TCCACGAGCTCAAGATCTGAGTGGCTGACCTGAGCGACCGCAACAGCTGCAAGCTGCC 1179  
 DB 321 AlaSerIleLeuGlnTyrLeuLysValProLeuValAspArgAlaThrCysLeuArgSer 340  
 QY 1180 AGCAGCTTCATCATCACCCAGAACATGTTCTGTGCGGCTACGACACCAACAGCAGGAGAT 1239  
 DB 341 ThrLysPheSerIleTyrSerHisMetPheCysAlaGlyTyrHisGluGlyGlyLysAsp 360  
 QY 1240 GCCTGCCAGGGGACAGCGGGGGCGCGACCTGACCCCGCTCAAGGACACCTACTTCGTG 1299  
 DB 361 SerCysGlnGlyAspSerGlyGlyProHisValThrGluValGluGlyTyrSerPheLeu 380  
 QY 1300 ACAGCATCGTCAGCTGGGAGAGAGCTGTGCTCCCGTAAGGGAAAGTACGGGATCTACACC 1359  
 DB 381 ThrGlyIleIleSerTrpGlyGluCysAlaMetLysGlyLysTyrGlyIleTyrThr 400  
 QY 1360 AAGTCTACCGCTCTCTCAAGTGGATCGACAGGTCATGAA 1401  
 DB 401 LysValSerArgTyrValAsnTrpIleLysGluLysThrLys 414  
 DB 401 LysValSerArgTyrValAsnTrpIleLysGluLysThrLys 414

RESULT 10





82 GlyAspGlnCysGluSerAsnProCysLeuAsnGlyGlyIleCysLysAspAspIleSer 101  
319 GAATACACCTGCACCTGTTTAAAGGATTCAAGAGCAAAACCTGTAATATTACACAGG 378  
102 SerTyrGluCysTrpCysGlnValGlyPheGluGlyArgAsnCysGluLeu-----Asp 119  
379 AAGTCTCTGACGCTGGACACGGGACTGTGACAGATTCTGC-----CACGAGGAACACAA 435  
120 AlaThrCysAsnIleLysAsnGlyArgCysLysGlnPheCysLysAsnSerProAspAsn 139  
436 TCTGTGTGCTCTCTGCGCCCGGGGTACACCTGCTGTGACACGGCAGCGCTGCAATT 495  
140 LysValIleCysSerCysThrGluGlyTrpGlnLeuAlaGluAspGlnLysSerCysGlu 159  
496 CCCACAGGCGCTTACCTCTGTGGAAACAGACCTGGAACCGCAGGAAGAGTCACTGGCC 555  
160 ProThrValProPheProCysGlyArgAlaSerIleSerTyrSerSerLysLysIleThr 179  
556 CAGGCCACACG-----AGCAGCGGGGAGGCC----- 582  
180 ArgAlaGluThrValPheSerAsnMetAspTyrGluAsnSerThrGluAlaValPheIle 199  
593 CCGTACACATCATGCAAGCCATATGATCCACCGCAGCTGACCCACCGACCGAACCC 642  
200 GlnAspAspIleThr-----AspGlyAlaIleLeuAsn----- 210  
643 TTCGACCTGCTTGAATCAACACGACGACGCTCAGAGGGCGGACAAACCTCACCAGG 702  
211 -----AsnValThrGluSerSerGluSerLeuAsnAspPheThrArg 224  
703 ATCGTGGAGCGCAGGAATGCAAGACGGGAGGTGCTCCGTGGAGCGCTGCTCATCAAT 762  
225 ValValGlyGlyGluAsnAlaLysProGlyGlnIleProTrpGlnValIleLeu---Asn 243  
763 GAGGAAACAGAGGTTCTGTGGTGGAACTATTCTGACGAGTCTACATCTCAACCGCA 822  
244 GlyGluIleGluAlaPheCysGlyAlaIleIleAsnGluIleValIleValAla 263  
823 GCCCACTGCTCTACCAAGCAAGATTCAGGTGAGGTGAGGCGGACCGGACACCGAG 882  
264 AlaHisCysLeuLysProGlyAspLysIleGluValAlaGlyGluTyrAsnIleAsp 283  
883 CAGGAGGAGCGGTGAGCGGTCACAGGTGAGGTGTCATCAAGCAACCGGTTCC 942  
284 LysLysGluAspThrGluGlnArgArgAsnValIleArgThrIleProHisHisGluTyr 303  
943 -----ACAAAGGAGACCTATGATCTGCACATCGCTGCTCGCGCTCAAGACCCCATC 996  
304 AsnAlaThrIleAsnLysTyrSerHisAspIleAlaLeuGluLeuAspLysProLeu 323  
997 ACCTTCGCGATGAACGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056  
324 IleLeuAsnSerTyrValThrProIleCysValAlaAsnArgGluTyrThr---AsnIle 342  
057 CTGATGACGACAGAGCGGATGTCAGCGGCTGCGGCGCACCACCGAGAGCGCGG 1116  
343 PheLeuLysPheGlySerGlyTyrValSerGlyTrpGlyLysValPheAsnLysGlyArg 362  
1117 CAGTCCACGAGCTCAAGATCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1176  
363 HisAlaSerIleLeuGluTyrLeuArgValProLeuValAspArgAlaThrCysLeuArg 382  
1177 TCCAGCAGCTTCATCATCACCAGACATGTTCTGTGCGCGCTACGACACCAAGCAGGAG 1236  
383 SerThrThrPheThrThrTyrAsnMetPheCysAlaGlyTyrArgGluGlyGlyLys 402  
1237 GATCGCTCCAGGCGGACAGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1296  
403 AspSerCysGluGlyAspSerGlyProHisValThrGluValGluGlyThrSerPhe 422  
297 GTGACGAGCTGTCAGTGGGAGAGAGCTGTGCGCGTAAAGGGAAGTACGGGATCTAC 1356  
423 LeuThrGlyIleIleSerIleTrpGlyGluGluCysAlaMetLysGlyLysTyrGlyIleTyr 442

QY 1357 ACCAAGTCACCCCTCTCTCAAGTCGATCGACAGTCATGAAA 1401  
Db 443 ThrLysValSerArgTyrValAsnTrpIleLysGluLysThrLys 457

## RESULT 8

FA9\_CANFA STANDARD; PRT; 452 AA.  
AC P19540; 1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).  
GN F9.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=90311364; PubMed=2367529;  
RA Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.;  
RT "Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic dogs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=89323338; PubMed=27521110;  
RA Evans J.P., Watzke H.H., Ware J.L., Stafford D.W., High K.A.;  
RT "Canine hemophilia B resulting from a point mutation with unusual consequences.";  
RL Blood 74:207-212(1989).  
RN [3]  
RP VARIANT HEMOPHILIA B GLU-418.  
RX MEDLINE=90099303; PubMed=2481310;  
RA Evans J.P., Brinkhous K.M., Brayer G.D., Reisner H.M., High K.A.;  
RT "Canine hemophilia B resulting from a point mutation with unusual consequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).  
CC -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA(2+) IONS, PHOSPHOLIPIDS, AND FACTOR VIIIa.  
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to form factor Xa.  
CC -1- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIa, WHICH EXCISES THE ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.  
CC -1- DISEASE: HEMOPHILIA B IS DUE TO DEFECTS IN FACTOR IX.  
CC -1- MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE, BEYOND THE GLA DOMAIN.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: Contains 2 EGF-like domains.  
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: M21757; AAA75006.1; -.  
CC DR EMBL: M33826; AAA30844.1; -.  
CC DR PIR: A30351; A30351.  
CC DR HSP: P00740; 1CFH.  
CC DR MEROPS: S01.214; -.  
CC DR InterPro: IPR001152; Asx\_hydroxyl.  
CC DR InterPro: IPR001314; Chymotrypsin.  
CC DR InterPro: IPR000742; EGF\_2.  
CC DR InterPro: IPR001881; EGF\_Ca.







RT [4] SEQUENCE FROM N.A.  
 RP MEDLINE=83220788; PubMed=6687940;  
 RA Jaye M., de la Salle H., Schamber F., Balland A., Kohli V.,  
 RA Finelli A., Tolstoshev P., Lecocq J.P.;  
 RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a  
 RT unique 52-base synthetic oligonucleotide probe deduced from the amino  
 RT acid sequence of bovine factor IX.";  
 RL Nucleic Acids Res. 11:2325-2335(1983).  
 RP [5]  
 RP SEQUENCE FROM N.A., AND VARIANTS THR-194 AND PRO-461.  
 RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
 RA Rajkumar N.R., Toth E.J., Yi O., Nickerson D.A.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 RP [6]  
 RP SEQUENCE OF 36-326 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=84300526; PubMed=6089357;  
 RA Jagaleswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;  
 RT "Isolation and characterization of human factor IX cDNA:  
 RT identification of Tq I polymorphism and regional assignment.";  
 RL Somat. Cell Mol. Genet. 10:465-473(1984).  
 RP [7]  
 RP SEQUENCE OF 290-359 FROM N.A.  
 RX MEDLINE=86127096; PubMed=3340835;  
 RA Stoffet E.S., Koebler D.D., Sarkar G., Sommer S.S.;  
 RT "Genomic amplification with transcript sequencing.";  
 RL Science 239:491-494(1988).  
 RP [8]  
 RP SEQUENCE OF 444-461 FROM N.A.  
 RX MEDLINE=94054330; PubMed=8236150;  
 RA de la Salle C., Charmanier J.L., Baas M.J., Schwartz A.,  
 RA Wiesl M.L., Grunebaum L., Cazenave J.-P.;  
 RT "A cletion located in the 3' non translated part of the factor IX  
 RT gene responsible for mild haemophilia B.";  
 RL Thromb. Haemost. 70:370-371(1993).  
 RP [9]  
 RP SEQUENCE OF 47-461 (VARIANT NAGOYA).  
 RX MEDLINE=90078229; PubMed=2592373;  
 RA Sueliro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,  
 RA Ogata K., Kamiya T., Saito H., Niho Y., Iwanaga S.;  
 RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by  
 RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell  
 RT chymase.";  
 RL J. Biol. Chem. 264:21257-21265(1989).  
 RP [10]  
 RP HYDROXYLATION OF ASP-110.  
 RX MEDLINE=83308813; PubMed=6688526;  
 RA McMullen B.A., Fujikawa K., Kisiel W.;  
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
 RT K-dependent blood coagulation zymogens.";  
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
 RP [11]  
 RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=78194509; PubMed=659613;  
 RA Di Sipio R.G., Kurachi K., Davie E.W.;  
 RT "Activation of human factor IX (Christmas factor).";  
 RL J. Clin. Invest. 61:1528-1538(1978).  
 RP [12]  
 RP CALCIUM-BINDING DATA.  
 RX MEDLINE=84185715; PubMed=6425296;  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RT "Derivatives of blood coagulation factor IX contain a high affinity  
 RT Ca2+ binding site that lacks gamma-carboxyglutamic acid.";  
 RL J. Biol. Chem. 259:5698-5704(1984).  
 RP [13]  
 RP ERRATUM.  
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
 RL J. Biol. Chem. 260:2583-2583(1985).  
 RP [14]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE.  
 RX MEDLINE=86189947; PubMed=3009023;  
 RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;

RT "Defective propeptide processing of blood clotting factor IX caused  
 RT by mutation of arginine to glutamine at position -4.";  
 RL Cell 45:343-348(1986).  
 RP [15]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=90062160; PubMed=2511201;  
 RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimonishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RP [16]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RP [17]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-107.  
 RX MEDLINE=92388094; PubMed=1517205;  
 RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;  
 RT "Human factor IX has a tetrasaccharide O-glycosidically linked to  
 RT serine 61 through the fucose residue.";  
 RL J. Biol. Chem. 267:17520-17525(1992).  
 RP [18]  
 RP PHOSPHORYLATION OF SER-114.  
 RA Harris R.J., Papac D.I., Truong L., Smith K.J.;  
 RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";  
 RL (In) Abstracts of Xith international conference on methods in protein  
 RL structure analysis, pp.50-50, Annecy (1996).  
 RP [19]  
 RP POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=20575397; PubMed=11133752;  
 RA Arruda V.R., Hagstrom J.N., Deitch J., Heiman-Patterson T.,  
 RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,  
 RA Larson P.J., High K.A.;  
 RT "Posttranslational modifications of recombinant myotube-synthesized  
 RT human factor IX.";  
 RL Blood 97:130-138(2001).  
 RP [20]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=95229607; PubMed=7713897;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane  
 RT binding region of factor IX by two-dimensional NMR spectroscopy.";  
 RL J. Biol. Chem. 270:7980-7987(1995).  
 RP [21]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=96032604; PubMed=7547952;  
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
 RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich  
 RT domain of factor IX.";  
 RL Biochemistry 34:12126-12137(1995).  
 RP [22]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=96279169; PubMed=8663165;  
 RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,  
 RA Furie B.;  
 RT "Identification of the phospholipid binding site in the vitamin K-  
 RT dependent blood coagulation protein factor IX.";  
 RL J. Biol. Chem. 271:16227-16236(1996).  
 RP [23]  
 RP STRUCTURE BY NMR OF 47-93.  
 RX MEDLINE=97199336; PubMed=9047312;  
 RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,  
 RA Smith H., Hickey R.G., Pedersen L.G.;  
 RT "Refinement of the NMR solution structure of the  
 RT gamma-carboxyglutamic acid domain of coagulation factor IX using  
 RT molecular dynamics simulation with initial Ca2+ positions determined  
 RT by a genetic algorithm.";

FT DISCFID 72 81 BY SIMILARITY. 376 18e-61 Length: 376  
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 FT CAREHYD 186 186 N-LINKED (GLCNAC...).  
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Alignment Scores:  
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 QY 181 ACCTGCTCATACGAAGAGGCGCGAGGTCTTTGAGGACAGGACGACGAAGTGAATTC 240  
 DB 21 LysCysSerLysGluGluAlaArgGluValPheLysAsnGluLysThrGluThrPhe 40  
 QY 241 TGGAAATTAATCAAGATGGGACCATGTGTGAGACCATGCTCTGCCAAGACCGGCAAA 300  
 DB 41 TrpAsnValTyrValAspGlyAspGlnCysSerSerAsnProCysHisTyrArgGlyThr 60  
 QY 301 TGTAAGAGCGCCGCGGGAATACACCTGCACCTGTTTGAAGATTCGAGGCAAAAC 360  
 DB 61 CysLysAspGlyIleGlySerTyrThrCysThrCysLeuProAsnTyrGluGlyLysAsn 80  
 QY 361 TGTGAATATTACACGAAGAGCTCTGCAGGCTTGACACCGGGAGCTGTGACCACTCTGC 420  
 DB 81 CysGluLysValLeuTyrGlnSerCysArgValAspAsnGlyAsnCysTyrPhePheCys 100  
 QY 421 CACGAGGACAGAACTCTGTGCTGTCTCTGCGCCCGGGGTACACCTCGCTGACAAAC 480  
 DB 101 LysArgValGlnSerGluThrGlnCysSerCysAlaGluSerTyrArgLeuGlyValAsp 120  
 QY 481 GGCAAGGCTGATTCACAGAGGCGCTACCCCTGTGGGAAACAGACCCCTGGAACGAGG 540  
 DB 121 GlyHisSerCysValAlaGluGlyAspPheSerCysGlyArgAsnIleLysAlaArgasn 140  
 QY 541 AAGAGGTGAGTGGCCCGAGCCACAGCAGCAGCGGGGAGCCCTGTGACATCATGAG 600  
 DB 141 Lys----- 141  
 QY 601 AAGCCATATGATGAGCGGACCTGGAGCCACCGAGAACCCCTTCGACCTGCTGACTTC 660  
 DB 141 ----- 141  
 QY 661 AACGAGCGCAGCCTGAGAGGGGGCGCAACAACCTCACCAGGATCGTGGGAGCCAGGAA 720  
 DB 142 ----- 142  
 QY 721 TGCAAGGACGGGAGTCTCCCTGCGAGCCCTGCTCATCAATGAGGAAACAGGGGTTC 780  
 DB 148 CysLysLeuGlyGluCysProTyrGlnAlaValLeuIleAsnGluLysGlyGluValPhe 167  
 QY 781 TGTGCTGGAATATTCTGACGGAGTCTACATCTTACGGCAGCCACCTCTCTACCAA 840  
 DB 168 CysGlyGlyThrIleLeuSerProIleHisValLeuThrAlaAlaHisCysIleAsnGln 187  
 QY 841 GCCAAGAGATTCAAGGTGAGGGTAGGGGACCGGACCGGACAGGAGGAGGCGGTGAG 900  
 DB 111 ----- 111

188 ThrLysSerVallys-----GluThrArgArgLeuLeu 198  
 QY 901 GCGGTCCACGAGGTGGAGGTGTCATCAAG-----CAC 933  
 DB 199 SerValAspLysIleTyrValHisThrLysPheValProAsnTyrTyrValHis 218  
 QY 934 AACCGTTTCCAAAGAGAGACCTATGACTTCGACATCGCGTCTCGCGTCAAGACCC 993  
 DB 219 GlnAsnPheAspArgValAlaTyrAspTyrAspIleAlaIleArgMetLysThrPro 238  
 QY 994 ATCACCTTCGGATGACGAGTGGCGCTGCTGCTCCCGGACGCTGACGCGCCAGTCC 1053  
 DB 239 IleGlnPheSerGluAsnValValProAlaCysLeuProThrAlaAspPheAlaAsnGlu 258  
 QY 1054 ACCTGATGACGACGAAGACGGGATTTGTAGCGGTCTCGCGGCGCACCCACGAGAGGCG 1113  
 DB 259 ValLeuMetLysGlnAspSerGlyIleValSerGlyPheGlyArgIleGlnPheLysGln 278  
 QY 1114 CGGCACTCCACGAGGCTCAAGATGTGTGAGGTGCGCTACGTGCGACCGCAACAGCTGCAAG 1173  
 DB 279 ProThrSerAsnThrLeuLysValIleThrValProTyrValAspArgHisThrCysMet 298  
 QY 1174 CTGTCACGAGCTTCATCATCACCAGAACATGTTCTGTGCGCGCTACGACACCAAGCAG 1233  
 DB 299 LeuSerSerAspPheArgIleThrGlnAsnMetPheCysAlaGlyTyrAspThrLeuPro 318  
 QY 1234 GAGGATGCTCGCAGGGGACAGCGGGGCGCGCAGCTCACCGCTTCAAGGACACCTAC 1293  
 DB 319 GlnAspAlaCysGlnGlyAspSerGlyGlyProHisIleThrAlaTyrArgAspThrHis 338  
 QY 1294 TTCGTGACAGGATCGTCAAGTGGGAGAGAGCTGTGCGGTAAAGGGGAGTACGGGATC 1353  
 DB 339 PheIleThrGlyIleIleSerTyrGlyGluGlyCysAlaArgLysGlyLysTyrGlyVal 358  
 QY 1354 TACACCAAGCTCACCCCTTCCTCAAGTGCAGTCGACAGCTCCATGAAACACGAGG 1407  
 DB 359 TyrThrLysValSerLysPheIleProTyrIleLysLysIleMetSerLeuLys 376

RESULT 6  
 ID FA9\_HUMAN STANDARD; PRT; 461 AA.  
 AC P00740;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).  
 GN F9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86000558; PubMed=2994716;  
 RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;  
 RT "Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).";  
 RL Biochemistry 24:3736-3750(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85190593; PubMed=3857619;  
 RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,  
 RA Graham J.B., Stafford D.W.;  
 RT "Evidence for a prevalent dimorphism in the activation peptide of human coagulation factor IX";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84236100; PubMed=6329734;  
 RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,  
 RA Huddleston J.A., Brownlee G.G.;  
 RT "The gene structure of human anti-haemophilic factor IX";  
 RL EMBO J. 3:1053-1060(1984).

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QY 637 AACCCCTTCGACCTGCTTACCTTCAACAGACGACGCTGAGAGGGGGCAACAACCTC 696
DB   |||   ...   |||   |||   |||   |||   |||   |||   |||   |||
QY 213 GluValPheThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 232
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 697 -----ACCAGGATCGTGGAGGCCAGGAAATGCAAGGACGGGAGGT 738
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 233 ThrAspProAsnValAspThrArgIleValGlyGlyAspGluCysArgProGlyGlyCys 252
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 739 CCTGGCAGGCGCTCTCATCATCATGAGGAAACAGGAGGTTCTGTGGTGGAACTATTCG 798
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 253 ProTyrGlnAlaValLeuIleAsnGluLysGlyGluPheCysGlyGlyThrIleLeu 272
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 799 ACGGAGTTTCATCCTTAACGCGACCCACTCTCTACCAAGCAGCAAGAGATTCAGGTG 858
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 273 AsnGluAspPheIleLeuThrAlaAlaHisCysIleAsnGlnSerLysGluIleLysVal 292
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 859 AGGTAGGAGCCGGAACAGGAGGAGGAGGCGGTGAGCGGTCACAGAGTGGAG 918
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 293 ValValGlyGluValAspArgGluLysGluGluHisSerGluThrThrHisThrAlaGlu 312
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 919 GTGGTCATCAACGACACCGGTTCCAAAGGAGACCTATGACTTCGACATGCCGTGCTC 978
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 313 LysIlePheValHisSerLysTyrIleAlaGluThrTyrAspAsnAspIleAlaLeuIle 332
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 979 CGGCTCAACAGCCCATCATCATCCCTCCGATGAACGTCGCGCTCCCGGCGGT 1038
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 333 LysLeuLysGluProIleGlnPheSerGluTyrValValProAlaCysLeuProGlnAla 352
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 1039 GACTGGCGGAGTCCACGCTGATGACGAGGAGGAGGATGTGAGCGGTCTCGGCGGC 1098
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 353 AspPheAlaAsnGluValLeuMetAsnGlnLysSerGlyMetValSerGlyPheGlyArg 372
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 1099 ACCCAGGAGAGGCGCGGAGTCCACGAGTCCAGAGTCTGAGGTCCTACGTGGAC 1158
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 373 GluPheGluAlaGlyArgLeuSerLysArgLeuLysValLeuGluValProTyrValAsp 392
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 1159 CGCAACAGCTGCAAGGTGTCACGAGCTTCATCATCACCCAGAACATGTCTGTGCCGCG 1218
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 393 ArgSerThrCysLysGlnSerThrAsnPheAlaIleThrGluAsnMetPheCysAlaGly 412
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 219 TAGCACACACGAGGAGATCCCTCCAGGCGGACAGCGGGGCGGCGGCGACGTACCCGC 1278
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 413 TyrGluThrGluGlnLysAspAlaCysGlnGlyAspSerGlyGlyProHisValThrArg 432
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 279 TTCAGGACACCTACTCTGTGACAGCATCGTCAGCTGGGAGAGAGCTGTGCCGTAA 1338
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 433 TyrLysAspThrTyrPheValThrGlyIleValSerTyrGlyGlyCysAlaArgLys 452
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 339 GGAAGTACGGGATCTACACCAAGTTCACCGCTTCCTCAAGTGGATCGACAGGTCCATG 1398
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 453 GlyLysTyrGlyValTyrThrLysLeuSerArgPheLeuArgTyrValArgThrValMet 472
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 399 AAACACAGG 1407
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
QY 473 ArgGlnLys 475
DB   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||

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RESULT 5

FA10\_TROCA

ID: FA10\_TROCA

AC: P81418;

DT: 30-May-2000 (Rel. 39, Created)

DT: 30-May-2000 (Rel. 39, Last sequence update)

DT: 28-Feb-2003 (Rel. 41, Last annotation update)

DE: Coagulation factor X (EC 3.4.21.6) (Trocarnin prothrombin activator).

OS: Tropidochis carinatus (Australian rough-scaled snake).

OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC: Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC: Elapidae; Notochidae; Tropidochis.

OX: NCBI TaxID=100989;

RN: [1]

RP: SEQUENCE, AND CHARACTERIZATION.

RC: Tissue=Venom;

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RX MEDLINE=99326314; PubMed=10397729;
RA Joseph J.S., Chung M.C.M., Jeyaseelan K., Kini R.M.;
RT "Amino acid sequence of trocarnin, a prothrombin activator from
RT Tropidochis carinatus venom: its structural similarity to coagulation
RT factor Xa.";
RL Blood 94:621-631(1999).
CC -!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting. Acts as a toxin
CC in venom.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -!- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.
CC -!- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC HSSP; P00742; 1HCG.
DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_III.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGF_BLOOD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYPSIN; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Zymogen; EGF-like domain; Repeat.
FT CHAIN 1 141 FACTOR X LIGHT CHAIN.
FT NON_CONS 141 142 FACTOR X HEAVY CHAIN.
FT CHAIN 142 376 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT CHAIN 142 376 EGF-LIKE 1, CALCIUM-BINDING.
FT DOMAIN 50 81 EGF-LIKE 2.
FT DOMAIN 89 124 SERINE PROTEASE.
FT DOMAIN 142 376 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 32 32 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 63 63 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 183 183 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 229 229 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 326 326 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 17 22 BY SIMILARITY.
FT DISULFID 50 61 BY SIMILARITY.
FT DISULFID 55 70 BY SIMILARITY.

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121	CysGluProValThrArgLysLeu	CysSerLeuAspAsnGlyGlyCysAspGlnPhe	Cys 140
1421	CACGAGGAACAGAACTCTGCTGTGTGCTCTCTGCGCCCGGGGTACACCTGGCTCACAAC	480	
141	LysGluGluGluAsnSerValLeu	CysSerCysAlaSerGlyThrLeuGlyAspAsn	160
481	GGCAAGGCGTCGATTTCCACAGAGGCGCCCTACCCCTGTGGGAAACAGACACCTGGAACGCGAGG	540	
161	GlyLysSerCysIleSerThrGluLeuPheProCysGlyLysValThrLeuGlyArgTrp	180	
541	AAGAGTTCAGTGGCCCGACGCCACACAGCAGCAGCGGGGAGGCCCTTCAGCATCATCATTGG	600	
181	ArgArgSer-----ProAlaThrAsnSerSerGluGlyProProGluAlaProGlyPro	198	
601	AAGCCATATGATGACGCGACCTGACGCCACCGAGAACCCCTTCGACCTGCTTCACATTC	660	
199	GluGlnGlnAspGlyAsnLeuThrAlaThrGluAsnProPheAsnLeuLeuAspSer	218	
661	AACCAGACGACGCTGAGAGGGCGACAAACCTCACCATGATCTGGGAGGCCAGGAA	720	
219	ProGluProProGluAspSerSerSerLeuValArgIleValGlyGlyGlnAsp	238	
721	TGCAGGAGCGGAGTGTCCTTCGGCAGGCCCTGCTCATCAATGAGGAAACACGAGGTTTC	780	
239	CysArgAspGlyGluCysProTrpGlnAlaLeuLeuValAsnGluGluAsnGlyPhe	258	
781	TGTGTGGAACTATTCTGAGCGAGTCTACATCTTAACGGCAGCCACTGTCTCTACCAA	840	
259	CysGlyGlyThrIleLeuSerGluThrHisValLeuThrAlaAlaHisCysLeuHisGln	278	
841	GCCAAAGAGATTCAAGGTGAGGTAGGGGACCGGAAACACGAGCAGGAGGAGCGGTGAG	900	
279	AlaLysArgPheLysValArgValGlyAspArgAspThrGluHisGluThrGlyAsnGlu	298	
901	GGGTGCCACGAGTGGAGGTGGTTCATCAGCAGCACACCGGTTTACAAAGGAGACCTATGAC	960	
299	GluThrHisGluValGluValValLysHisAsnArgPheValLysGluThrTyrrasp	318	
961	TTCCAGATCCGCTGCTCCGGCTCAAGACGCCCATCACCTCCGATGAACCTGGCGCT	1020	
319	PheAspIleAlaValLeuArgLeuLysThrProIleThrPheArgArgAsnValAlaPro	338	
1021	GCTGCTCCCGAGCGTGACTGGGCGGAGTCCACGCTGATGACGACGAGACGCGGATT	1080	
339	AlaCysLeuProGlnLysAspTrpAlaGluSerThrLeuMetAlaGlnLysThrGlyIle	358	
081	GTGAGCGGCTGGGGGCACCCACGAGAGGGCGCGCAGTCCACAGGCTCAAGATGCTG	1140	
359	ValSerGlyPheGlyArgThrHisGluMetGlyArgLeuSerThrThrLeuLysMetLeu	378	
1141	GAGTGCCCTAGTGACCGCCAAACAGCTGCTCAAGCTCCAGAGCTTCATCATCACCCAG	1200	
379	GluValProTyrrValAspArgAsnSerCysLysArgSerSerPheThrIleThrGln	398	
201	ACATGTTCTGTGCGCGGTACGACACCAACAGAGGAGGATGCTGCCAGGGGACGCGGG	1260	
399	AsnMetPheCysAlaGlyTyrraspAlaArgProGluAspAlaCysGlnGlyAspSerGly	418	
1261	GGCCCGCAGTCAACCGCTTCAAGGACACTTACTGTCGACAGGCATCTGAGCTGGGA	1320	
419	GlyProHisValThrArgPheArgaspThrTyrrPheValThrGlyIleValSerTrpGly	438	
1321	GAGAGCTGTGCCGTAAAGGGGAAGTACGGGATCTACCAAGGTACCACGCTTCCTCAAG	1380	
439	GluGlyCysAlaArgLysGlyLysPheGlyValTyrrLysValSerAsnPheLeuLys	458	
381	TGGATCGACAGGTTCATGAAACACGAGGGCTTGCCCAAGGCCAAGAGC	1428	
459	TrpIleGluSerMetArgAlaArgAlaValProValAlaGluAla	478	

ID	FA10_BOVIN	STANDARD;	PRT;	492 AA.
AC	P00743;			
AD	21-JUL-1986 (Rel. 01, Created)			
AT	13-AUG-1987 (Rel. 05, Last sequence update)			
DDT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).			
GN	F10.			
OS	Bos taurus (Bovine).			
OC	Eumkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OC	NCBI_TaxID=9913;			
RN	[1]			
RN	SEQUENCE OF 1-487 FROM N.A.			
RN	MEDLINE=84247315; PubMed=6330671;			
RN	Fung M.R., Campbell R.M., McGillivray R.T.A.;			
RA	"Blood coagulation factor X mRNA encodes a single polypeptide chain			
RA	containing a prepro leader sequence.";			
RT	Nucleic Acids Res. 12:4481-4492(1984).			
RT	[2]			
RN	SEQUENCE OF 41-180.			
RN	MEDLINE=80130563; PubMed=6766735;			
RA	Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,			
RA	Titani K.;			
RT	"Amino acid sequence of the light chain of bovine factor X1 (Stuart			
RT	factor).";			
RL	Biochemistry 19:659-667(1980).			
RL	[3]			
RN	REVISION TO 103.			
RN	MEDLINE=83308813; PubMed=6688526;			
RA	McMullen B.A., Fujikawa K., Kisiel W.;			
RA	"The occurrence of beta-hydroxyaspartic acid in the vitamin			
RT	K-dependent blood coagulation zymogens.";			
RT	Biochem. Biophys. Res. Commun. 115:8-14(1983).			
RL	[4]			
RN	SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS			
RN	MEDLINE=76053069; PubMed=1059093;			
RA	Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,			
RA	Neurath H.;			
RT	"Bovine factor X1 (Stuart factor): amino-acid sequence of heavy			
RT	chain.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).			
RL	[5]			
RN	SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.			
RN	MEDLINE=94062825; PubMed=8243461;			
RA	Inoue K., Morita T.;			
RA	"Identification of O-linked oligosaccharide chains in the activation			
RT	peptides of blood coagulation factor X. The role of the carbohydrate			
RT	moieties in the activation of factor X.";			
RL	Eur. J. Biochem. 218:153-163(1993).			
RL	[6]			
RN	ACTIVE SITE.			
RN	MEDLINE=73053314; PubMed=4264286;			
RA	Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,			
RA	Neurath H., Davie E.W.;			
RT	"Bovine factor X la (activated Stuart factor). Evidence of homology			
RT	with mammalian serine proteases.";			
RL	Biochemistry 11:4899-4903(1972).			
RL	[7]			
RN	PROCESSING.			
RN	MEDLINE=76053121; PubMed=1059122;			
RA	Fujikawa K., Titani K., Davie E.W.;			
RA	"Activation of bovine factor X (Stuart factor): conversion of factor			
RT	Xa-alpha to factor Xa-beta.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).			
RL	[8]			
RN	CALCIUM-BINDING DATA.			
RN	MEDLINE=84185716; PubMed=6546930;			
RA	Sugo T., Bjoerk I., Holmgren A., Stenflo J.;			
RA	"Calcium-binding properties of bovine factor X lacking the gamma-			
RT	carboxyglutamic acid-containing region.";			
RT	J. Biol. Chem. 259:5705-5710(1984).			
RL	[9]			







RC RX MEDLINE-86221713; PubMed-3011603;  
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
RT "Isolation and characterization of human blood-coagulation factor X  
RT cDNA";  
RL Gene 41:311-314(1986).  
RN [6]  
RP SEQUENCE OF 41-179.  
RX MEDLINE-83257207; PubMed-6871167;  
RA McGee B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,  
RA Kwa J.Y., Weinstein B.;  
RT "Complete amino acid sequence of the light chain of human blood  
RT coagulation factor X: evidence for identification of residue 63 as  
RT beta-hydroxyaspartic acid.";  
RL Biochemistry 22:2875-2884(1983).  
RN [7]  
RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
RC TISSUE-LIVER;  
RX MEDLINE-84222026; PubMed-6587384;  
RA Leyland S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;  
RT "Characterization of a cDNA coding for human factor X";  
RL Proc Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
RN [8]  
RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE-94062825; PubMed-8243461;  
RA Inoue K., Morita T.;  
RT "Identification of O-linked oligosaccharide chains in the activation  
RT peptides of blood coagulation factor X. The role of the carbohydrate  
RT moieties in the activation of factor X";  
RL Eur. J. Biochem. 218:153-163(1993).  
RN [9]  
RP SEQUENCE OF 1-23 FROM N.A.  
RX MEDLINE-90128299; PubMed-2612918;  
RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;  
RT "Cloning and characterization of the 5' end (exon 1) of the gene  
RT encoding human factor X";  
RL Gene 84:517-519(1989).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
RX MEDLINE-93360277; PubMed-8355279;  
RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
RA Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;  
RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
RL J. Mol. Biol. 232:947-966(1993).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
RX MEDLINE-98283982; PubMed-9618463;  
RA Kanaka K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
RT "Structural basis for chemical inhibition of human blood coagulation  
RT factor Xa.";  
RL Proc Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
RN [12]  
RP VARIANTS ILE-7 AND HIS-30.  
RX MEDLINE-99318093; PubMed-10391209;  
RA Cardall M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nimesh J., Ziaugra L.,  
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
RA Lander E.S.;  
RT "Characterization of single-nucleotide polymorphisms in coding regions  
RT of human genes";  
RL Nat. Genet. 22:231-238(1999).  
RN [13]  
RP ERRATUM.  
RA Cardall M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nimesh J., Ziaugra L.,  
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
RA Lander E.S.;  
RL Nat. Genet. 23:373-373(1999).  
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
CC converts prothrombin to thrombin in the presence of factor Va,  
CC calcium and phospholipid during blood clotting.  
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
CC Arg-|-Ile bonds in prothrombin to form thrombin.

CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
CC MORE DISULFIDE BONDS.  
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
CC CALCIUM.  
CC -1- PTM: N- AND O-GLYCOSYLATED.  
CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: Contains 2 EGF-like domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: K03194; AAA52490.1; -  
CC EMBL: M57285; AAA52421.1; -  
CC EMBL: AF503510; AM19347.1; -  
CC EMBL: L29433; AAA52764.1; -  
CC EMBL: L00390; AAA52764.1; JOINED.  
CC EMBL: L00391; AAA52764.1; JOINED.  
CC EMBL: L00392; AAA52764.1; JOINED.  
CC EMBL: L00393; AAA52764.1; JOINED.  
CC EMBL: L00394; AAA52764.1; JOINED.  
CC EMBL: L00395; AAA52764.1; JOINED.  
CC EMBL: L00396; AAA52764.1; JOINED.  
CC EMBL: M22613; AAA51984.1; -  
CC EMBL: K01886; AAA52486.1; -  
CC EMBL: M33297; AAA52636.1; -  
CC PIR: A24478; EXHU.  
CC PDB: 1HCG; 08-MAY-95.  
CC PDB: 1FAX; 29-OCT-97.  
CC PDB: 1FXI; 17-JUN-98.  
CC PDB: 1XKA; 23-MAR-99.  
CC PDB: 1XKB; 23-MAR-99.  
CC PDB: 1EZO; 20-SEP-00.  
CC PDB: 1FOR; 20-SEP-00.  
CC PDB: 1FOS; 20-SEP-00.  
CC PDB: 1FJS; 17-NOV-00.  
CC PDB: 1G2L; 20-OCT-01.  
CC PDB: 1G2M; 20-OCT-01.  
CC PDB: 1KSN; 19-JUN-02.  
CC PDB: 1KYE; 11-FEB-03.  
CC PDB: 1MQ5; 28-JAN-03.  
CC PDB: 1MQ6; 28-JAN-03.  
CC PDB: 1NFU; 25-FEB-03.  
CC PDB: 1NFW; 25-FEB-03.  
CC PDB: 1NFX; 25-FEB-03.  
CC PDB: 1NFX; 25-FEB-03.  
CC MEROPS: S01.216; -  
CC GlycoSuiteDB: P00742; -  
CC Genew: HGNC:3528; F10.  
CC MIM: 134530; -  
CC MIM: 227600; -  
CC GO: GO:0005576; C:extracellular; TAS.  
CC GO: GO:0003804; F:blood coagulation; TAS.  
CC GO: GO:0007596; P:blood coagulation; TAS.  
CC InterPro: IPR000152; Asx\_hydroxyl.  
CC InterPro: IPR001314; Chymotrypsin.  
CC InterPro: IPR000742; EGF 2.  
CC InterPro: IPR001881; EGF Ca.  
CC InterPro: IPR001438; EGF II.  
CC InterPro: IPR006209; EGF-like.  
CC InterPro: IPR002383; GLA blood.  
CC InterPro: IPR001254; Ser. protease\_Try.  
CC InterPro: IPR000294; vitk\_dep\_GLA.  
CC Pfam: PF00008; EGF; 2.

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 11, 2003, 10:30:05 ; Search time 30.5 Seconds  
(without alignments)  
4523.815 Million cell updates/sec

Title: US-09-632-722-1

Perfect score: 2713

Sequence: 1 atgggggcccacgcacct.....cgctctctccattaaagtga 1467

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 255726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_n2p.model -DEV=xlp  
-O=/usr2/spool/US09632722/runat\_11082003\_093234\_23853/app\_query.fasta\_1.1607  
-DB=SwissProt\_41 -FMF=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMF=PO -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09632722 @CGN.1.1.37 @runat\_11082003\_093234\_23853 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIME=UT-120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT= -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

SwissProt\_41.\*

Print: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2630	96.9	488	1 FA10_HUMAN	P00742 homo sapien
2	1949	71.8	490	1 FA10_RABIT	O19045 oryctolagus
3	1851	68.2	492	1 FA10_BOVIN	P00743 bos taurus
4	1425	52.5	475	1 FA10_CHICK	P25155 gallus gall
5	135.5	41.9	376	1 FA10_TROCA	P81428 tropidechis
6	1041.5	38.4	461	1 FA9_HUMAN	P00740 homo sapien
7	1039.5	38.3	459	1 FA9_MOUSE	P16294 mus musculus
8	1032.5	38.1	452	1 FA9_CANFA	P19540 canis famli
9	963	35.5	416	1 FA9_BOVIN	P00741 bos taurus
10	954	35.2	444	1 FA7_RABIT	P98139 oryctolagus
11	948	34.9	466	1 FA7_HUMAN	P08709 homo sapien
12	89.5	33.5	446	1 FA7_MOUSE	P70375 mus musculus
13	872	32.1	407	1 FA7_BOVIN	P22457 bos taurus
14	872	32.1	456	1 PRTC_BOVIN	P00745 bos taurus
15	861	31.7	461	1 PRTC_RAT	P31394 rattus norv
16	858	31.6	461	1 PRTC_MOUSE	P33587 mus musculus
17	853.5	31.5	459	1 PRTC_PIG	Q9gip2 sus scrofa
18	829.5	30.6	458	1 PRTC_RABIT	Q28661 oryctolagus

19	827	30.5	461	1 PRTC_HUMAN	P04070 homo sapien
20	637	23.5	622	1 THRB_HUMAN	P00734 homo sapien
21	621.5	22.9	618	1 THRB_MOUSE	P19221 mus musculus
22	598.5	22.1	625	1 THRB_BOVIN	P00735 bos taurus
23	594.5	21.9	617	1 THRB_RAT	P18292 rattus norv
24	585.5	21.6	*400	1 PRTC_HUMAN	P22891 homo sapien
25	568	20.9	275	1 FA9_RABIT	P16292 oryctolagus
26	566	20.9	282	1 FA9_RAT	P16296 rattus norv
27	559.5	20.6	285	1 FA9_CAVPO	P16295 cavia porce
28	544.5	20.1	271	1 FA9_PIG	P16293 sus scrofa
29	521	19.2	274	1 FA9_SHEEP	P16291 ovis aries
30	510	18.8	396	1 PRTC_BOVIN	P00744 bos taurus
31	437.5	16.1	559	1 TPA_RAT	P19637 rattus norv
32	429	15.8	559	1 TPA_MOUSE	P11214 mus musculus
33	427	15.7	786	1 STUB_DROME	O05319 drosophila
34	417	15.4	562	1 TPA_HUMAN	P00750 homo sapien
35	415.5	15.3	247	1 TRY3_RAT	P12788 rattus norv
36	412	15.2	247	1 TRY4_RAT	P08426 rattus norv
37	408	15.0	686	1 MAS2_HUMAN	O00187 homo sapien
38	405	14.9	477	1 URT2_DESRO	P15638 desmodus ro
39	402.5	14.8	566	1 TPA_BOVIN	Q28198 bos taurus
40	401.5	14.8	434	1 UROK_CHICK	P15120 gallus gall
41	399.5	14.7	1019	1 LFC_TACTR	P28175 tachypleus
42	396	14.6	638	1 KAL_RAT	P14272 rattus norv
43	395.5	14.6	1019	1 LFC_CARRO	Q26422 carnoscor
44	394.5	14.5	231	1 TRY2_SALSA	P35032 salmo salar
45	393.5	14.5	455	1 TMS5_MOUSE	Q9er04 mus musculus

## ALIGNMENTS

RESULT 1	FA10_HUMAN	STANDARD;	PRT;	488 AA.
ID	FA10_HUMAN			
AC	P00742; Q14340;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).			
GN	F10.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91216473; PubMed=1902434;			
RA	Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;			
RT	"Cloning and expression in COS-1 cells of a full-length cDNA encoding			
RT	human coagulation factor X.;"			
RL	Gene 99:291-294(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87026600; PubMed=3768336;			
RA	Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;			
RT	"Gene for human factor X: a blood coagulation factor whose gene			
RT	organization is essentially identical with that of factor IX and			
RL	Biochemistry 25:5098-5102(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,			
RA	Ozuna M., Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE OF 13-488 FROM N.A.			
RX	MEDLINE=85216545; PubMed=2582420;			
RA	Fung M.R., Hay C.W., McGillivray R.T.A.;			
RT	"Characterization of an almost full-length cDNA coding for human			
RT	blood coagulation factor X.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).			
RN	[5]			
RP	SEQUENCE OF 19-488 FROM N.A.			



QY	309	GTCAGCTGGGGAGAGAGCTGTGCCGTAAGGGGAAGTACGGGATCTACACCAAGGTCACC	1368
Db	141	ValSerTrpGlyGluGlyCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThr	160
QY	369	GCC	1371
Db	161	Ala	161

Search completed: August 11, 2003, 10:50:06  
Job time 81 secs

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196 GAGCGCGGAGGTCCTTTGAGGACAGCGACAGCAAGCAATGAATTCGGAATAAATCAAA 255
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67 GluAlaGlnGluIlePheGlnAsnValGluAspThrLeuAlaPheTrpIleLysTyrPhe 86
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256 GATGCCACCAAGTGTAGACC-----AGTCCTTCCCAAGAAC 291
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87 AspGlyaspGlnCysSerAlaProProLeuAspHisGlnCysAspSerProCysGly 106
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292 CAGGCAAAATGTAAGACGCGCTCGGGGAATACACCTGCACCTGTTTAGAAGATTTCGAA 351
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107 HisGlyThrCysIleAspGlyIleGlySerPheSerCysSerCysAspLysGlyTrpGlu 126
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352 GCGAAAACCTGTGAATTTATTCACACGG---AAGCTCTGCAGCCTGGACACAGCGGACTGT 408
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127 GlyLysPheCysGlnGlnGluLeuArgPheGlnAspCysArgValAsnAsnGlyGlyCys 146
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
409 GACCAGTCTGCCACGAGGACAGAACTCTGTGGTGTCTCTCCGCGCGCGGTACACC 468
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
147 LeuHisTyrCysLeuGluIleSerAsnGlyArgCysAlaCysAlaProGlyTyrGlu 166
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
469 CTGGCTGACAAACGCGAGGCTTCATCCACAGGCGCTTACCCCTGTGGGAAA-----522
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 LeuAlaAspAspHisMetArgCysLysSerThrValAsnPheProCysGlyLysLeuGly 186
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
523 CAGACCTGGAACGCGAGGAGAGGTGAGTGGCCCGCAGCCACACAGCAGCGGGGAGGCC 582
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187 ArgTrpIleGluLysLysArgLysIleLeuLysArgAspThr-----200
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
583 CCTGACAGCATCATGGAAGCATATGATGACAGCGAGCTGGAGCCACCAGACCC 642
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200 -----200
643 TTGCAGCTGCTTACCTAACAGCAGACGACCTGAGAGGGGCGACAAACCTCACAGG 702
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201 ---AspLeuGluAspGluLeuGluProAspPro-----Arg 211
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703 ATCGTGGAGGCGCAGGAATCAAGGACGCGGAGTGTCCCTGGCAGCGCTGTCATCAT 762
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212 IleValAsnGlyThrLeuThrLysGlnGlyAspSerProTrpGlnAlaIleLeuLeuAsp 231
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763 GAGGAAACGAGGTTTCTGTGTGGAAGTATCTCTGAGCGAGTCTACATCCCTAACGGCA 822
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232 SerLysLysLysLeuAlaCysGlyGlyValLeuIleHisThrSerTrpValLeuThrAla 251
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823 GCCCACTGCTCTACCAAGCCAGACATTCAAGGTGAGGTGAGGACCGGACCAACAGCGAG 882
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252 AlaHisCysValGluGlyThrLysLysLeuThrValArgLeuGlyGlyTrpAspLeuArg 271
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883 CAGGAGGAGGCGGTGAGGCGGTGCACGAGGTGAGGTGTCATCAAGCACACACCGGTTC 942
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272 ArgArgAspHisTrpGluLeuAspLeuAspIleLysGluIleLeuValHisProAsnTyr 291
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943 ACAAGAGACCTATGACTTCGACATCGCGTCTCCGCTCAAGACCCCATCATCCTTC 1002
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292 ThrArgSerSerSerAspAsnAspIleAlaLeuLeuArgLeuAlaGlnProAlaThrLeu 311
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332 GlnAlaGlyGlnGluThr---ValValThrGlyTrpGlyTyrGlnSerAspArgIleLys 350
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117 CAGTCCACCAAG-----CTCAAGATGCTGGAGGTGCCCTTACGTGGACCGC 1161
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351 AspGlyArgArgAsnArgThrPheIleLeuThrPheIleArgIleProLeuValAlaArg 370
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162 AACAGCTGCAAGCTGTCCAGCAGCTCATCATCACCAGAACATGTTCTGTCCCGCGCTAC 1221
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371 AsnGluCysValGluValMetLysAsnValValSerGluAsnMetLeuCysAlaGlyIle 390
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QY 1222 GACACCAAGCAGGAGGATCCCTGCCAGGGGACAGCGGGGCCCCCAGCTACCCGCTTC 1281
Db 391 IleGlyAsnThrArgAspAlaCysAspGlyAspSerGlyGlyProMetValValPhePhe 410
QY 1282 AAGGACACCTACTCTGTCACAGGATCGTCAGCTGGGAGAGAGCTGTGCCCGTAAGGG 1341
Db 411 ArgGlyThrTrpPheLeuValSerTrpGlyGluGlyCysGlyHisThrAsn 430
QY 1342 AAGTACGGGATCTACACCAAGGTCAACCGCTCTCTCAAGTGGATCGACAGGTCCATGAA 1401
Db 431 AsnTyrGlyIleThrLysValGlySerTyrLeuLysTrpIleHisSerTyrIleGly 450
QY 1402 ACCAGGGGCTTG 1413
Db 451 GluLysGlyVal 454

RESULT 15
I62744
coagulation factor Xa (EC 3.4.21.6) - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C:Accession: I62744
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures
A:Reference number: I46196; MUID:94222160; PMID:8168596
A:Accession: I62744
A>Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-161 <RES>
A:Cross-references: GB:D21214; NID:9415307; PIDN:BAA04755.1; PID:9455395
C:Superfamily: coagulation factor X; BGF homology; Gla domain homology; trypsin homol
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F:1-161/Domain: trypsin homology (fragment) <TRY>

Alignment Scores:
Pred. No.: 1,65e-42 Length: 161
Score: 837.00 Matches: 156
Percent Similarity: 98.14% Conservative: 2
Best Local Similarity: 96.89% Mismatches: 3
Query Match: 30.85% Indels: 0
DB: 2 Gaps: 0

US-09-632-722-1 (1-1467) x I62744 (1-161)

QY 889 GAGGCGGTGAGGCGGTGCACGAGGTGAGGTGTCATCAAGCACACCGGTTCAACAAG 948
Db 1 GluGlyGlyGluAlaValHisGluValGluValIleLysHisAsnArgPheThrLys 20
QY 949 GAGACCTATGACTTCGACATCGCGTGTCCGGCTCAAGACCCCATCATCCTCCGATG 1008
Db 21 GluThrTyrAspPheAspIleAlaValLeuArgLeuLysSerProIleThrPheArgMet 40
QY 1009 AACGTGGCGCTGCTGCTCCCGAGGTGACGTGAGTGGCGGAGTCCAGCTGATCACCAG 1068
Db 41 AsnValAlaProAlaCysLeuProGluArgAspTrpAlaGluSerThrLeuMetThrGln 60
QY 1069 AAGACGGGGATTGTACGCGGCTTCGGCGCGACCCACAGAGAGGCGCGCAGTCCACAGG 1128
Db 61 LysThrGlyIleValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArg 80
QY 1129 CTCAGATGCTGGAGGTGCCCTACGTGGACCGCGCAACAGCTGCAAGCTGTCCAGCAGTTC 1188
Db 81 LeuLysMetLeuGluValProTyrValAspArgAsnSerCysLysLeuSerSerPhe 100
QY 1189 ATCATCACCCCAACAATGTTCTGTGCGCGCTTACGACACCAAGCAGGAGGAGTCCCTGCCAG 1248
Db 101 IleIleThrGlnAsnMetPheCysAlaGlyTyrHisAlaLysGlnGluAspAlaCysGln 120
QY 1249 GGGGACAGCGGGGCGCGCGAGCTCACCCTGTTCAAGGACACCTACTTCTGTCAGAGGCATC 1308
Db 121 GlyAspSerGlyGlyProHisValThrArgPheLysAspThrTyrPheValThrGlyIle 140

```







QY 649 CTGCTTGACTTCAACGAGCAGCGCCTGAGAGGGGCGACAAACCTCACAGGATCGTG 708  
 Db |||||  
 152 -----ArgileVal 154  
 QY 709 GGAGGCCAGGAATGCAAGACGCGGGAGTGCTCCCTGGCAGGCCCTGCTCATCAATGAGAA 768  
 Db |||||  
 155 GlyGlyHisValCysProLysGlyGluCysProTrpGlnAlaMetLeu---LysLeuAsn 173  
 QY 769 AACGAGGCTTCTGGTGGAGTACTTCTGACGAGTCTCATCTCAACGCCAGCCAC 828  
 Db |||||  
 174 GlyAlaLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 193  
 QY 829 TGTCTCTACCAAGCAAGAGATCAAGGTGAGG-----GTAGGGGAC 870  
 Db |||||  
 194 CysPhe-----GluArgLeuArgSerArgGlyAsnLeuThrAlaValLeuGlyGlu 210  
 QY 871 CGGACAGGACGAGGAGGAGGCGGTGAGGGGTGCACAGGTGGAGGTGCTCATCAAG 930  
 Db |||||  
 211 HisAspLeuSerArgValGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 230  
 QY 931 CACAAACCGGTTCCACAAAGAGACCTATGCTTCGACATCGCGTCTCCGCTCAAGACC 990  
 Db |||||  
 231 ProLysGlnTyrValProGlyClnThrAspHisValAlaLeuLeuGlnLeuAlaGln 250  
 QY 991 CCATACCTCCGATCAACGATCGCGCTGCTCCCTCCCGAGCGTGAAGTGGCCGAG 1050  
 Db |||||  
 251 ProValAlaLeuGlyAspHisValAlaProLeuCysLeuProAspPheAlaAsp 270  
 QY 051 TCCAGCTCATCAGCAGAGAGCGGGATTGAGCGGCTTCGCGGCGCACCCAGAGAG 1110  
 Db |||||  
 271 GlnThrLeuAlaPheValArgPheSerAlaValSerGlyTrpGlyGlnLeuGluArg 290  
 QY 111 GCGCGGCTCCACAGGCTCAAGATGCTGGAGGTGCTTACGTCAGCGCGCACCGAG 1170  
 Db |||||  
 291 GlyValThrAlaArgLysLeuMetValValLeuValProArgLeuThrGlnAspCys 310  
 QY 171 AAGCTGTCCAGC-----AGCTTCATCATCACCAGCAAGATGTCGTGTC 1215  
 Db |||||  
 311 LeuGlnGlnSerArgGlnArgProGlyGlyProValValThrAspAsnMetPheCysAla 330  
 QY 216 GCTACGACCAACGAGGAGATGCTCCAGGGGACAGCGGGGCGCGCGCACGTCACC 1275  
 Db |||||  
 331 GlyTyrSerAspGlySerLysAspAlaCysLysGlyAspSerGlyGlyProHisAlaThr 350  
 QY 276 CGCTTCAAGGACCACTTCTGTCAGGATCGTCAGTGGGAGAGAGTGTGCCCGT 1335  
 Db |||||  
 351 ArgPheArgGlyThrTrpPheLeuThrGlyValValSerTrpGlyGluGlyCysAlaAla 370  
 QY 336 AAGGGAGTACGGATCTACACCAAGGTCCACCGCTTCCCTCAAGTGTGATCGACAGTCC 1395  
 Db |||||  
 371 AlaGlyHisPheGlyIleTyrThrArgValSerArgTyrThrAlaTrpLeuArgGlnLeu 390  
 QY 396 ATGAAACCAAGGGGCTTGGCCCAAGGCAAG 1425  
 Db |||||  
 391 Met-----GlyHisProSerArg 397

# RESULT 12 KXBO

protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)  
 N:Alternative names: autoprothrombin IIA; plasma protein C  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 3-Nov-1980 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999  
 C:Accession: A26250; A18385; A18386; A00928  
 R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984.  
 A:Title: Cloning and sequence of liver cDNA coding for bovine protein C.  
 A:Reference number: A26250; MUID:85014826; PMID:6091100  
 A:Accession: A26250  
 A:Molecule type: mRNA  
 A:Residues: 1-456 <LON>  
 J:Bernlund, P.; Stenflo, J.  
 J. Biol. Chem. 257, 12170-12179, 1982  
 A:Title: Amino acid sequence of the light chain of bovine protein C.

A:Reference number: A18385; MUID:83007325; PMID:6896876  
 A:Accession: A18385  
 A:Molecule type: protein  
 A:Residues: 40-194 <PER>  
 A:Note: 82-Lys was also found  
 R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983  
 A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.  
 A:Reference number: A19316; MUID:83169769; PMID:6572939  
 A:Contents: annotation; revision to residue 110  
 R:Stenflo, J.; Fernlund, P.  
 J. Biol. Chem. 257, 12180-12190, 1982  
 A:Title: Amino acid sequence of the heavy chain of bovine protein C.  
 A:Reference number: A18386; MUID:83007326; PMID:6896877  
 A:Accession: A18386  
 A:Molecule type: protein  
 A:Residues: 197-454, PV <STE>  
 R:Esmon, N.L.; Debault, L.E.; Esmon, C.T.  
 J. Biol. Chem. 258, 5548-5553, 1983  
 A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless  
 A:Reference number: A37541; MUID:83213513; PMID:6304092  
 A:Contents: annotation; activation; calcium binding  
 R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.  
 J. Biol. Chem. 258, 5554-5560, 1983  
 A:Title: Structural changes required for activation of protein C are induced by Ca<sup>2+</sup>  
 A:Reference number: A37542; MUID:83213514; PMID:6406503  
 A:Contents: annotation; activation; calcium binding  
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that  
 S:Comment: Protein C is synthesized in the liver as a single chain precursor, which i  
 bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this re  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s  
 cognition of the thrombin-thrombomodulin complex.  
 C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium bind  
 F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:30-39/Domain: propeptide #status predicted <PRO>  
 F:40-194/Product: protein C light chain #status experimental <LCH>  
 F:98-128/Domain: EGF homology <EG1>  
 F:137-172/Domain: EGF homology <EG2>  
 F:197-456/Product: protein C heavy chain #status experimental <HCH>  
 F:197-210/Domain: activation peptide #status experimental <APT>  
 F:211-440/Domain: trypsin homology <TRY>  
 F:45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #s  
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #s  
 F:136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:252,298,397/Active site: His, Asp, Ser #status predicted  
 F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
 Pred. No.: 1,36e-44 Length: 456  
 Score: 872.00 Matches: 183  
 Percent Similarity: 56.24% Conservative: 83  
 Best Local Similarity: 38.69% Mismatches: 155  
 Query Match: 32.14% Indels: 52  
 DB: 1 Gaps: 10

US-09-632-722-1 (1-1467) x KXBO (1-456)

QY 64 GAAGTCTGTTTCATCCGAGGAGCAGCAGCAACATCTCTGGAGGGTCCAGAGGCC 123  
 Db |||||  
 21 AspSerValPheSerSerSerGlnArgAlaHisGlnValLeuArgLysArgAla 40  
 QY 124 AATTCCTTCTTGAAGAGATCAAGAAAGGACACCTCCAAAGAGAGTGCATGGAGACCC 183  
 Db |||||  
 41 AsnSerPheLeuGluGluLeuArgProGlyAsnValGluArgGluCysSerGluGluVal 60  
 QY 184 TGCTCATACGAAGAGCCCGAGGTCTTTGAGGACAGCAGCAGCAATGAATTCCTGG 243  
 Db |||||  
 61 CysGluPheGluGluAlaArgGluPheGlnAsnThrGluAspThrMetAlaPheTrp 80

QY 667 AGCGAGCTGAGAGGGCGGCAACAACCTCACCAGGATCGTGGGAGGCCAGGAATGCAAG 726  
Db |||||||  
QY 727 GACGGGAGTGTCCCTGCGAGCCCTGCTCATCATGAGGAACAGGGTTCCTGGT 786  
Db |||||||  
QY 200 LysGlyGluCysProTrpGlnAlaLeuMetAsnGlySerThrLeu---LeuCysGly 218  
QY 787 GAACTATTCCTGAGCGAGTCTTACATCTCAACGCGAGCCCACTGT-----CTCTAC 837  
Db |||||||  
QY 219 GlySerLeuLeuAspThrHisTrpValSerAlaAlaHisCysPheAspLysLeuSer 238  
QY 838 CAAGCCAGACATCAAGGTGAGGTGAGGACCGGACACAGGAGGAGGAGGCGGT 897  
Db |||||||  
QY 239 SerLeuArgAsnLeuThrIleValLeuGlyGluHisAspLeuSerGluHisGluGlyAsp 258  
QY 898 GAGCGGTGTCAGGAGTGTGTCATCAAGCACACACCGGTTCCAAAGAGGACCTAT 957  
Db |||||||  
QY 259 GluGlnValArgHisValAlaGlnLeuMetProAspLysTrpValProGlyLysThr 278  
QY 958 GACTTCGACATCGCGTCTCGGCTCAAGACCCCATCACTTCCGCATGAGCGTGGC 1017  
Db |||||||  
QY 279 AspHisAspIleAlaLeuLeuArgLeuLeuGlnProAlaAlaLeuThrAsnValVal 298  
QY 018 CCTGCTCCCTCCCGAGCGTACTGGCGGAGTCCAGCTGATGACGACGAGGAGCGGG 1077  
Db |||||||  
QY 299 ProLeuCysLeuProGluArgAsnPheSerGluSerThrLeuAlaThrIleArgPheSer 318  
QY 078 ATTGTGAGCGCTTCGGCGGCGCACCCAGAGAGGCGCGGTCACACGAGCTCAAGATG 1137  
Db |||||||  
QY 319 ArgValSerGlyTrpGlnLeuLeuTrpArgGlyAlaLeuAlaArgGluLeuMetAla 338  
QY 138 CTGAGGTGCGCTACGTGGAGCCGACAGCTGCAAGCTGTCCAGC-----1182  
Db |||||||  
QY 339 IleAspValProArgLeuMetThrGlnAspCysValGluGlnSerGluHisAsnProGly 358  
QY 183 AGCTTCATCATCCAGACATGTTCTGTCCGGCTACGACACCAAGAGGAGTGC 1242  
Db |||||||  
QY 359 SerProGluValThrGlyAsnMetPheCysAlaGlyTrpLeuAspGlySerLysAspAla 378  
QY 243 TGCCAGGGGACAGCGGGGCGCCGACGTCACCGCTTCAAGGACACTCTTCGTGACA 1302  
Db |||||||  
QY 379 CysLysGlyAspSerGlyGlyProHisAlaThrSerTrpHisGlyThrTrp---LeuThr 397  
QY 303 GGCATGCTCAGCTGGGAGAGAGCTGTCCCGTAAGGGGAGTACGGGATCTACCAAG 1362  
Db |||||||  
QY 398 GlyValValSerTrpGlyGlyGlyCysAlaArgValGlyHisValGlyValTrpArg 417  
QY 363 GTCACCGCTTCCCTCAAGTGGATGCGACAGCTCCATGAAACACAGG 1407  
Db |||||||  
QY 418 ValSerArgAspThrGluTrpLeuSerArgLeuMetArgSerLys 432

## RESULT 11

KFE07  
coagulation factor VIIa (EC 3.4.21.21) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 2-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999  
C:Accession: A31979; C20274  
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.  
J. Biol. Chem. 263, 14868-14877, 1988  
A:Title: Bovine factor VII. Its purification and complete amino acid sequence.  
A:Reference number: A31979; MUID:89008362; PMID:3049594  
A:Accession: A31979  
A:Molecule type: protein  
A:Residues: 1-407 <TAK>  
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor VII.  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Accession: C20274  
A:Molecule type: protein  
A:Residue: 58-62, 'X', 64-68 <MCM>  
A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J. Biochem. 104, 867-868, 1988  
A:Title: A new triscarboxylate sugar chain linked to a serine residue in bovine blood coagulation factor VIIa. MUID:89213999; PMID:3149637  
A:Contents: annotation  
A:Note: structure and location of covalently bound carbohydrate  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor  
A:Pathway: blood coagulation extrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid; coagulation factor VIIa light chain #status experimental <MAL>  
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MAL>  
F:1-44/Domain: Gla domain homology (fragment) <GLA>  
F:50-81/Domain: EGF homology <EGF>  
F:91-127/Domain: EGF homology <EG2>  
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F:153-387/Domain: trypsin homology <TRY>  
F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
F:17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-343/Modified site: carboxyglutamic acid (Glu) #status experimental  
F:52/Binding site: carboxyglutamic acid (Ser) (covalent) #status experimental  
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental  
F:145-203/Binding site: carboxyglutamic acid (Ser) (covalent) #status experimental  
F:152-153/Cleavage site: Arg-Ile (coagulation factor VIIa) #status experimental  
F:193-242,344/Active site: His, Asp, Ser #status predicted  
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

## Alignment Scores:

Pred. No.:	1,36e-44	Length:	407
Score:	872.00	Matches:	174
Percent Similarity:	54.44%	Conservative:	71
Best Local Similarity:	38.67%	Mismatches:	137
Query Match:	32.14%	Indels:	68
DB:	1	Gaps:	9

US-09-632-722-1 (1-1467) x KFE07 (1-407)

QY 121 GCAATTCCTTCTTGAAGAGATGAAGAAAGACACCTCGAAAGAGAGATGCAATGGAAG 180  
Db 1 AlaAsnGlyPheLeuGluGluLeuLeuProGlySerLeuGluArgGlyCysArgGluGlu 20  
QY 181 ACCTGCTCATAGAGAGCGCCGCGAGGTCTTTGAGGACAGGACAGCAAGCAATGAATC 240  
Db |||||||  
QY 21 LeuCysSerPheGluGluAlaHisGluIlePheArgAsnGluGluArgThrArgGlnPhe 40  
QY 241 TGAATAATAACAAAGATGGCGACCATGTGAGACCATGCTTCCCTGCGAGACACGAGGCA 300  
Db |||||||  
QY 41 TrpValSerTrpAsnAspGlyAspGlnCysAlaSerSerProCysGlnAsnGlyGlySer 60  
QY 301 TGTAAGAGCGCTCGGGGAATACACCTCTGTCACCTCTTTAGAGAGATTCGAAGGCAAAAC 360  
Db 61 CysGluAspGlnLeuArgSerTrpIleCysPheCysProAspGlyPheGluGlyArgAsn 80  
QY 361 TGTGATTA-----TTACACGGAAGCTCTGCACCTGACACAGCGGAGCTGTGACACG 414  
Db |||||||  
QY 81 CysGluThrAspLysGlnSerGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100  
QY 415 TTCTGCGCAGGAGCAACAACTCT---GTGGTGTCTCTCTGCGCCGCGGCTACACCTG 471  
Db |||||||  
QY 101 TyrCysGlyAlaAspProGlyAlaGlyArgPheCysTrpCysHisGluGlyTrpAlaLeu 120  
QY 472 GCTGACACGGAAGAGGCTGATTCCTCCAGGGCCCTACCCCTGTGGGAAA---CAGACC 528  
Db |||||||  
QY 121 GlnAlaAspGlyValSerCysAlaProThrValGluTrpCysGlyLysIleProVal 140  
QY 529 CTGGACACGGAAGAGGCTGATTCCTCCAGGGCCCTACCCCTGTGGGAAA---CAGACC 588  
Db |||||||  
QY 141 LeuGluLysArgAsnGlySerLysProGlnGly-----151  
QY 589 AGCATCATGGAAGCCCATATGATGACGCGCAGCTGGACCCACCGAGAACCCCTTCGAC 648  
Db 151 -----151











337 AlaAspLysGluTyrThr---AsnIlePheLeuLysPheGlySerGlyTyrValSerGly 355  
090 TTCGGGGCCAGCCAGAGAGGGCGGCGGAGTCCACCGCTCAGATGCTGGAGTGGCC 1149  
356 TrpGlyArgValPheHisGlyGlyArgSerAlaLeuValLeuGlnTyrLeuArgValPro 375  
150 TACGTGGCCGCAACAGCTGCAAGCTGTCAGACGCTTCATCATCCACAGACATGTC 1209  
376 LeuValAspArgAlaThrCysLeuArgSerThrLysPheThrIleTyrAsnAsnMetPhe 395  
210 TGTGGCGGCTAGCAGACCAAGCAGGAGGATGCTCCAGGGGACAGCGGGGGCCGAC 1269  
396 CysAlaGlyPheHisGlyGlyArgSerCysGlnGlyAspSerGlyGlyProHis 415  
270 GTACCCGCTTCAAGACACCTACTGTCGACGATCGTCAGCTGGGAGAGAGCTGT 1329  
416 ValThrGluValGluGlyThrSerPheLeuThrGlyIleSerTrpGlyGluGluCys 435  
330 GCCGTGAAGGGAAGTACGGGATCTACACCAAGGTCACCGCTTCTCCTCAAGTGGATCGAC 1389  
436 AlaMetLysGlyLysThrGlyLeuThrLysValSerArgTyrValAsnTrpIleLys 455  
390 AGTCCATGAAA 1401  
456 GluLysThrLys 459  
RESULT 6  
JQ0419  
coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)  
C:Species Mus musculus (house mouse)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999  
C:Accession: JQ0419, I49667  
R:Wu, S.M.; Stafford, D.W.; Ware, J.  
Gene 86, 75-278, 1990  
A:Title: Reduced amino acid sequence of mouse blood-coagulation factor IX.  
A:Reference number: JQ0419; MUID:90215309; PMID:2323576  
A:Accession: JQ0419  
A:Molecule type: mRNA  
A:Residue: 1-459 <RUS>  
A:Cross-references: GB:M23109; NID:g193317; PIDN:AAA37629.1; PID:g387158  
R:Sarkar, G.; Koerber, D.D.; Sommer, S.S.  
Genomics, 133-143, 1990  
A:Title: Direct sequencing of the activation peptide and the catalytic domain of the fac  
A:Reference number: I46580; MUID:90152675; PMID:2303254  
A:Accession: I49667  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residue: 168-362, 'Q', 364-387, 'I', 389-451 <RES>  
A:Cross-references: GB:M26236; NID:g193319; PIDN:AAA37630.1; PID:g193320  
C:Comment: This protein plays a critical role in blood coagulation.  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>  
F:17-34/Domain: propeptide #status predicted <PRO>  
F:19-79/Domain: Gla domain homology <GLA>  
F:35-459/Domain: coagulation factor IX #status predicted <MAT>  
F:85-116/Domain: EGF homology <EGF>  
F:122-158/Domain: EGF homology <EG2>  
F:225-452/Domain: trypsin homology <TRY>  
F:41,42,43,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxyglutamic acid (Glu) #s  
F:52-57,89-96,90-105,107-122,133,129-143,145-158,166-333,250-266,380-394,405-433/DLS  
F:265,313-409/Active site: His, Asp, Ser #status predicted  
Alignment Scores:  
Pred. No Length: 459  
Score: 1039.50  
Percent Similarity: 60.84%  
Best Local Similarity: 44.42%  
Query Match: 38.32%  
DB: 2  
Gaps: 11  
US-09-632-722-1 (1-1467) x JQ0419 (1-459)

25 CTGCTCAGTGCCTCCCTGGCTGGCTCCTCTGCTGGGAA---AGTCTGTTCATCCGC 81  
2 LeuIleThrIlePheLeuLeuGlyTyrLeuLeuSerThrGluCysAlaValPheLeuAsp 21  
82 AGGAGCAGGCCCAACATCTCTGGCGAGGGTACAGGGCCAAATTC---TTCTTGA 138  
22 ArgGluAsnAlaThrLysIleLeuThrArgProLysArgTyrAsnSerGlyLysLeuGlu 41  
139 GAGATGAAGAAAGACACCTCGAAGAGAGTGAAGAGAGCTCTCATACGAGAG 198  
42 GluPheValArgGlyAsnLeuGluGluCysIleGluGluArgCysSerPheGluGlu 61  
199 GCCCGCAGGTCTTTGAGGACGACGACAAAGCAATGAATCTTGAATAAATAAAGAT 238  
62 AlaArgGluValPheGluAsnThrGluLysThrThrGluPheThrLysGlnTyrValAsp 81  
259 GCCGACAGTGTGACAGCAGTCTTCCAGACACCGAGGCAATGTAAGACGGCTCGG 318  
82 GlyAspGlnCysGluSerAsnProCysLeuAsnGlyGlyIleCysLysAspIleSer 101  
319 GAATACACCTGCACCTGTTTGAAGAGATTGGAAGGCAAAACTGTGAATATTACAC 378  
102 SerTyrGluCysTrpCysGlnValGlyPheGluGluArgAsnCysGluLeu-----Asp 119  
379 AAGCTCTGACCTGGACACACGGGACTGTGACAGTCTTCG---CAGGAGAACACAAC 435  
120 AlaThrCysAsnIleLysAsnGlyArgCysLysGlnPheCysLysAsnSerProAspAsn 139  
436 TCTGTGTGCTCTCTCGCCCGGGGTACACCTCGGTGACACGACGAGGCTGCTGAT 495  
140 LysValIleCysSerCysThrGluGlyTrpGlnLeuAlaGluAspGlnLysSerCysGlu 159  
496 CCCACAGGGCCCTACCCCTGTGGAAACACAGACCTTGAACGACGAGAGAGTCAAGTGC 555  
160 ProThrValProPheProCysGlyArgAlaSerIleSerTyrSerSerLysIleThr 179  
556 CAGGCCACACG---AGCAGCGGGAGGCG---582  
180 ArgAlaGluThrValPheSerAsnMetAspTyrGluAsnSerThrGluAlaValPheIle 199  
583 CTGACACATCAGATGAGCCATATGATGACGCGGACCTGGACCCACCCAGGAGAACCC 642  
200 GlnAspIleThr-----AspGlyAlaIleLeuAsn-----210  
643 TTCGACCTGCTGATTCACACGACGACGCTGAGAGGGGCGACAAACACCTCACAGG 702  
211 -----AsnValThrGluSerSerGluSerLeuAsnAspPheThrArg 224  
703 ATCTGGGAGGCGCAGGATGCAAGACGGGAGTCTCCCTGGCAGGCGCTGCTCATCAAT 762  
225 ValValGlyGlyGluAsnAlaLysProGlyGlnIleProTrpGlnValIleLeu---Asn 243  
763 GAGGAAACAGGAGGTTCTGTGGTGAATCTTTCAGCGAGTCTTACATCTCTAACGCA 822  
244 GlyGluIleGluAlaPheCysGlyGlyAlaIleAsnGluLysTrpIleValThrAla 263  
823 GCCCACTCTCTACCAAGCAAGAGATTCAGGTGAGGGTAGGGACCGGACACGAG 882  
264 AlaHisCysLeuLysProGlyAspLysIleGluValAlaGlyGluTyrAsnIleAsp 283  
883 CAGGAGGAGGCGGTGAGGCGGTGACGAGGTGGAGGTGTCATCAAGCACACCGGTTC 942  
284 LysLysGluAspThrGluGlnArgAsnValIleArgThrIleProHisGlnTyr 303  
943 -----ACAAAGGAGACCTATGACTTCGACATCGCGTCCGGCTCCAGACCCCATC 996  
304 AsnAlaThrIleAsnLysTyrSerHisAspIleAlaLeuLeuGluLeuAspLysProLeu 323  
997 ACCTTCGCGATGAACGTGGCGCTCCCTCCCTCCCGAGCTGCTGCGGCGGAGTCCAG 1056  
324 IleLeuAsnSerTyrValThrProIleCysValAlaAsnArgGluTyrThr----AsnIle 342





R:Kurachi, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982  
A:Title: Isolation and characterization of a cDNA coding for human factor IX.  
A:Reference number: A30623; MUID:83065193; PMID:6959130  
A:Accession: A30623  
A:Molecule type: mRNA  
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A'.  
A:Cross-references: GB:J00136; NID:9182608; PIDN:AAA98726.1; PID:9182609  
A:Experimental source: liver  
A:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.  
Vox Sang. 58, 21-29, 1990  
A:Title: Development of an immunocaffinity process for factor IX purification.  
A:Reference number: A60486; MUID:90194857; PMID:2316207  
A:Accession: A60486  
A:Molecule type: protein  
A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>  
A:R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Accession: A20274  
A:Molecule type: protein  
A:Residues: 105-109, 'X', 111-115 <MCW>  
A:R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la S.  
Eur. J. Biochem. 172, 565-572, 1988  
A:Title: Characterisation of two differently processed forms of human recombinant fac  
A:Reference number: S02527; MUID:88166735; PMID:3280312  
A:Accession: S02527  
A:Molecule type: protein  
A:Residues: 29-63 <BAL>  
A:Note: processed forms expressed in recombinant system  
A:R:Yallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulle  
EMBO J. 9, 3295-3301, 1990  
A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice  
A:Reference number: S12058; MUID:91006024; PMID:2209546  
A:Accession: S12058  
A:Molecule type: mRNA; protein  
A:Residues: 1-68 <JAL>  
A:Note: processed forms expressed in recombinant system  
A:R:Hardford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Cam  
EMBO J. 9, 475-480, 1990  
A:Title: The first EGF-like domain from human factor IX contains a high-affinity calc  
A:Reference number: S12377; MUID:90151623; PMID:2406129  
A:Accession: S12377  
A:Molecule type: protein  
A:Residues: 92-130 <HAN>  
A:Note: NMR detection of calcium binding by domain expressed in recombinant system  
R:de la Salle, C.; Charmantier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Gruneba  
Thromb. Haemost. 70, 370-371, 1993  
A:Title: A deletion located in the 3' non translated part of the factor IX gene respo  
A:Reference number: I59612; MUID:94054330; PMID:8236150  
A:Accession: I59612  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 444-461 <RES>  
A:Cross-references: GB:S66752; NID:9439773; PIDN:AAB28588.1; PID:9439774  
R:Stoflet, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.  
Science 239, 491-494, 1988  
A:Title: Genomic amplification with transcript sequencing.  
A:Reference number: I59529; MUID:88127096; PMID:3340835  
A:Accession: I59529  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 230-359 <RES>  
A:Cross-references: GB:W19063; NID:9182622; PIDN:AAA52456.1; PID:9182623  
R:Aqarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimomishi, Y.; Nishimura, H.  
Biochemistry 33, 5167-5171, 1994  
A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically  
A:Reference number: A54255; MUID:94227047; PMID:8172892  
A:Accession: A54255  
A:Molecule type: protein  
A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGA>  
A:Note: the residues designated 'X' were determined to be threonine bound to carbohy





361 TGTGAATATTACACGGAAGCTCTGCAGCGCTGCACAAACGGGACTGTGACCACTGCTGC 420  
 Db |||||  
 121 CysGluLeuPheValArgLysLeuCysSerLeuAspGlnGlySerPheLeuGlyAsnAsp 140  
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 421 CACGAGAACAACTCTGTGGTGTCTCTGGCGCCGGGTACACCCCTGGCTGACAAAC 480  
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 161 GlyLysSerCysLeuSerThrAlaProPheProCysGlyLysThrAsnLysGlyA-Gala 180  
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 541 AAGAGTCAGTGGCCCGCCAGCCACGACGAGCGGGGAGCGCCCTGCACAGCATCACATGG 600  
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 181 LysArgSerValAlaLeuAsnThrSerAsnSerGluProAspProGluAspLeuMet--- 199  
 Qy |||||  
 601 AAGCCATATGATGACGCGGACCTGGACCCACGAGAACCCCTGCACCTGCTGACTTC 660  
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 661 AACGACGAGCGCTGAGAGGGCGGCAACAACCTCACATCTACGACGACCCACCTGCTCTAC 837  
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 Qy |||||  
 958 GACTTCGACATCCCGTCTCCGGCTCAAGACCCCATCACCTTCGCGATGAACGTGGCG 1017  
 Db |||||  
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 Qy |||||  
 1018 CTTGCTGCTCCCGGAGCGTGTACTGGCGGAGTCCACGTGTATGACGAGAGCGGG 1077  
 Db |||||  
 338 ProAlaCysLeuProGlnLysAspTyrAlaGluAlaThrLeuMetThrGlnLysThrGly 357  
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 Qy |||||  
 1318 GGAGAGAGTGTGCGCGTGAAGGGAGTACGGGATCTACACCAAGTCCACCGCTTCCTC 1377  
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 Qy |||||  
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Db |||||  
 478 ThrHisProPro 481.  
 RESULT 3  
 EXBO  
 coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
 N:Alternate names: Stuart factor  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 24-Apr-1984 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999  
 C:Accession: A22867; A14997; A12030; A34412; S39414; A00925  
 R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.  
 Nucleic Acids Res. 12, 4481-4492, 1984  
 A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containin  
 A:Reference number: A22867; MUID:84247315; PMID:6330671  
 A:Accession: A22867  
 A:Molecule type: mRNA  
 A:Residues: 1-487 <FNU>  
 A:Cross-references: GB:X00673; NID:q192; PIDN:CAA25286.1; PID:q193  
 R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
 Biochemistry 19, 659-667, 1980  
 A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A:Reference number: A14997; MUID:80130563; PMID:6766735  
 A:Accession: A14997  
 A:Molecule type: protein  
 A:Residues: 41-102, 'N', 104-180 <ENF>  
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood  
 A:Reference number: A20274; MUID:83308813; PMID:6688526  
 A:Contents: annotation; revision to residue 103  
 R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
 A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A:Reference number: A12030; MUID:76053069; PMID:1059093  
 A:Accession: A12030  
 A:Molecule type: protein  
 A:Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492  
 R:Persson, E.; Selaender, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epiderm  
 A:Reference number: A34412; MUID:89580326; PMID:2789221  
 A:Accession: A34412  
 A:Molecule type: protein  
 A:Residues: 85-126 <PER>  
 A:Note: beta-hydroxyaspartic acid site  
 R:Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides  
 A:Reference number: S39414; MUID:94062825; PMID:8243461  
 A:Accession: S39414  
 A:Molecule type: protein  
 A:Residues: 183-196; 199-209; 216-233 <INO>  
 A:Note: carbohydrate binding sites  
 R:Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
 Biochemistry 11, 4899-4903, 1972  
 A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mamm  
 A:Reference number: A12453; MUID:73053314; PMID:4264286  
 A:Contents: annotation; active site  
 R:Fujikawa, K.; Titani, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha  
 A:Reference number: A13504; MUID:76053121; PMID:1059122  
 A:Contents: annotation; activation  
 R:Suigo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxygluta  
 A:Reference number: A38024; MUID:84185716; PMID:6546930  
 A:Contents: annotation; calcium binding  
 R:Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A:Reference number: A38025; MUID:86140210; PMID:3949800  
 A:Contents: annotation; sulfate binding



A:Residues: 19-284, 'E', 289-488 <KAU>  
A:Cross-References: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336  
R:Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A. 1985  
Proc. Nat. Acad. Sci. U.S.A. 82, 3591-3595  
A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor X.  
A:Reference number: A22208; MUID:85216545; PMID:2582420  
A:Accession: A22208  
A:Molecule type: mRNA  
A:Residues: 13-441, 'S', 443-488 <FUN>  
A:Cross-References: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841  
R:Leytus, S.P.; Chung, D.W.; Kiesel, W.; Kurachi, K.; Davie, E.W.  
Proc. Nat. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
A:Title: Characterization of a cDNA coding for human factor X.  
A:Reference number: A21284; MUID:84222026; PMID:6587384  
A:Accession: A21284  
A:Molecule type: mRNA  
A:Residues: 13-284, 'E', 289-488 <LE2>  
R:McMullen, B.A.; Fujikawa, K.; Kiesel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins  
Biochemistry 22, 2875-2884, 1983  
A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.  
A:Reference number: A20362; MUID:83257207; PMID:6871167  
A:Accession: A20362  
A:Molecule type: protein  
A:Residues: 41-179 <NCM>  
R:Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993  
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of human blood coagulation factor X.  
A:Reference number: S39414; MUID:94062825; PMID:8243461  
A:Accession: S39415  
A:Molecule type: protein  
A:Residues: 183-234 <INO>  
A:Note: glycosylation sites  
A:Note: Identification and characterization of beta-hydroxyaspartic acid  
R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusan, K.; Lyman, G.  
Gene 84, 517-519, 1989  
A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human blood coagulation factor X.  
A:Reference number: I54051; MUID:90128299; PMID:2612918  
A:Accession: I54051  
A:Status: translation not shown; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-23 <RES>  
A:Cross-References: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:G553330  
R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla  
J. Mol. Biol. 232, 947-966, 1993  
A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
A:Reference number: A49458; MUID:93360277; PMID:8355279  
A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
C:Comment: The two chains held together by one disulfide bond are formed from a single-c  
C:Genetic: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) of  
A:Gene: GB:F10  
A:Cross-References: GDB:119890; OMIM:227600  
A:Map position: 13q34-13q34  
A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
A:Note: efficiency of this factor causes Stuart disease  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keyword: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:41-179/Domain: coagulation factor X light chain #status experimental <LCH>  
F:90-121/Domain: EGF homology <EG1>  
F:129-164/Domain: EGF homology <EG2>  
F:183-488/Domain: coagulation factor X heavy chain #status experimental <HCH>  
F:183-234/Domain: activation peptide #status experimental <AP>  
F:235-488/Domain: coagulation factor Xa heavy chain #status experimental <ACT>  
F:235-462/Domain: trypsin homology <TRI>  
F:46,47,51,55,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
F:57-62/Disulfide bonds: #status predicted

F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-4  
E:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F:221,231/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #s  
F:276,322,419/Active site: His, Asp, Ser #status experimental

Alignment Scores:  
Pred. No.: 2,05e-149 Length: 488  
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Best Local Similarity: 99.80% Mismatches: 1  
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Db 21 GlyGluSerLeuPheIleArgArgGluGlnAlaAsnIleLeuAlaArgValThrArg 40  
QY 121 GCCAATTCCTTCTTGAAGAGATGAAGAAAGACACCTCGAAAGAGAGTGCATGGAAGAG 180  
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QY 421 CACGAGGAACAGAACTCTGT 480  
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QY 601 AAGCCATATGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
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Db 221 AsnGlnThrGlnProGluArgGlyAspAsnLeuThrArgIleValGlyGlyGlnGlu 240  
QY 721 TGAAGGAGGAGGAGTGTCTGT 780  
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GenCore version 5.1.6  
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OM nucleotide - protein search, using frame\_plus\_n2p model

Run on: August 11, 2003, 10:36:55 ; Search time 59 Seconds  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 566616

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database

PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2630	96.9	488	1 EXHU	coagulation factor
2	1957	72.1	482	1 EXRT	coagulation factor
3	1851	68.2	492	1 EXBO	coagulation factor
4	1425	52.5	475	1 EXCH	coagulation factor
5	1041.5	38.4	461	1 KFHU	coagulation factor
6	739.5	38.3	459	2 JQ0419	coagulation factor
7	732.5	38.1	452	1 A30351	coagulation factor
8	963	35.5	416	1 KFB07	coagulation factor
9	948	34.9	466	1 KFH07	coagulation factor
10	45.5	34.9	443	2 I46932	coagulation factor
11	872	32.1	407	1 KFB07	coagulation factor
12	862	32.1	456	1 KXBO	protein C (activat
13	861	31.7	461	1 S18994	protein C (activat
14	858	31.6	461	1 JX0210	protein C (activat

#### ALIGNMENTS

##### RESULT 1

EXHU coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N.Alternate names: Stuart factor  
C.Species: Homo sapiens (man)

C.Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #text\_change 08-Dec-2000  
C.Accession: A24478; JQ0917; A42485; A25853; A22208; A21284; A20362; S39415; I54051;

R.Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
Biochemistry 25, 5098-5102, 1986

A.Title: Gene for human Factor X: a blood coagulation factor whose gene organization  
A.Reference number: A24478; MUID:87026600; PMID:3768336

A.Accession: A24478  
A.Molecule type: DNA

A.Residues: 1-488 <LEV>

A.Cross-references: GB:L29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; PID:g182831  
R.Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.

Gene 99, 291-294, 1991

A.Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human c

A.Reference number: JQ0917; MUID:91216473; PMID:1902434

A.Accession: JQ0917

A.Molecule type: mRNA

A.Residues: 1-488 <MES>

A.Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390

R.Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.

J. Biol. Chem. 267, 7395-7401, 1992

A.Title: Liver-specific expression of the gene coding for human factor X, a blood coa

A.Reference number: A42485; MUID:92218390; PMID:1313796

A.Accession: A42485

A.Molecule type: DNA

A.Residues: 1-15 <MIA>

A.Experimental source: liver

A.Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBI:93787)

R.Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.

Gene 41, 311-314, 1986

A.Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A.Reference number: A25853; MUID:86221713; PMID:3011603

A.Accession: A25853

A.Molecule type: mRNA

coagulation factor  
protein C (activat  
coagulation factor  
thrombin (EC 3.4.2  
thrombin (EC 3.4.2  
thrombin (EC 3.4.2  
thrombin (EC 3.4.2  
plasma protein 2 p  
factor IX - rabbit  
coagulation factor  
coagulation factor  
factor IX - pig (f  
coagulation factor  
plasma protein 2 -  
t-plasminogen acti  
thrombin (EC 3.4.2  
polyprotein - Afri  
serine proteinase  
t-plasminogen acti  
plasma hyaluronan-  
t-plasminogen acti  
trypsin (EC 3.4.21  
trypsin (EC 3.4.21  
t-plasminogen acti  
Ra-reactive factor  
thrombin (EC 3.4.2  
thrombin (EC 3.4.2  
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u-plasminogen acti  
plasmin (EC 3.4.21









LOCATIONS: (43)....(461)  
 US-09-978 917A-2

Alignment Scores: 6.91e-45 Length: 461  
 Pred. No.: 827.00 Matches: 168  
 Score: 54.62% Conservativity: 92  
 Percent Similarity: 35.29% Mismatches: 160  
 Best Local Similarity: 30.48% Indels: 56  
 Query Match: 11 Gaps: 9  
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US-09-632-722-1 (1-1467) x US-09-978-917A-2 (1-461)

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 288 HisProAsnTyrSerLysSerThrThrAspAsnAspIleAlaLeuLeuHisLeuAlaGln 307  
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 308 ProAlaThrLeuSerGlnThrIleValProIleCysLeuProAspSerGlyLeuAlaGlu 327  
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 1105 GAGAAAGCGCGGAGTCCACGAG-----CTCAGATGCTGGAGGTGCC 1149  
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 387 CysAlaGlyIleLeuGlyAspArgGlnAspAlaCysGluGlyAspSerGlyGlyProMet 406  
 1270 GTCACCCCTTCAAGGACACCTACTTCTGTCAGGACATCTGTCAGTGGGAGAGAGCTGT 1329  
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 1330 GCCCGTAAGGGAACTACGAGTACACCAAGGTCACCGCTTCCTCAAGTGGATCGAC 1389  
 427 GlyLeuLeuHisAsnTyrGlyValTyrThrLysValSerArgTyrLeuAspTrpIleHis 446  
 1390 AGTGCTCATGAAACACAGGGGCTTGCCCAAGGCCAAGACCCATGCCCG 1437  
 447 GlyHisIleArgAspLysGluAlaProGln---LysSerTrpAlaPro 461

RESULT 14  
 US-10-182-263-2  
 ; Sequence 2, Application US/10182263  
 ; Publication NO. US20030022354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerlitz, Bruce E  
 ; APPLICANT: Jones, Bryan E  
 ; APPLICANT: Grinnell, Brian W  
 ; TITLE OF INVENTION: PROTEIN C DERIVATIVES  
 ; FILE REFERENCE: X-13611  
 ; CURRENT APPLICATION NUMBER: US/10182,263  
 ; PRIOR FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: 60/181948  
 ; PRIOR FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: 60/189199  
 ; PRIOR FILING DATE: 2000-03-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 461  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-182-263-2

Alignment Scores:  
 Pred. No.: 6.91e-45 Length: 461  
 Score: 827.00 Matches: 168  
 Percent Similarity: 54.62% Conservativity: 92  
 Best Local Similarity: 35.29% Mismatches: 160  
 Query Match: 30.48% Indels: 56  
 DB: 15 Gaps: 9

US-09-632-722-1 (1-1467) x US-10-182-263-2 (1-461)

931 CACAACCGGTTTCAAAAGGAGACCTATGACTTCACATCGCGGTGCTCCGGCTCAAGACC 990  
 288 HisProAsnTyrSerLysSerThrThrAspAsnAspIleAlaLeuLeuHisLeuAlaGln 307  
 991 CCCATCACCCTCCCGATGACGTCGGCGCTCCCTGCTCCCGGAGCGTACTGGCGCGAG 1050  
 308 ProAlaThrLeuSerGlnThrIleValProIleCysLeuProAspSerGlyLeuAlaGlu 327  
 1051 TCCACGCTG-----ATGACGACGAGACGCGGATTTGTGACGCTTCGGCGCGACCCAC 1104  
 328 ArgGluLeuAsnGlnAlaGlyGlnGluThr---LeuValThrGlyTyrHisSer 346  
 1105 GAGAAAGCGCGGAGTCCACGAG-----CTCAGATGCTGGAGGTGCC 1149  
 347 SerArgGluLysGluAlaLysArgAsnArgThrPheValLeuAsnPhelLysIlePro 366  
 1150 TACGTGGACCCACACAGCTGCAAGCTGTCCAGCAGCTTCATCATCACCCAGAACATGTC 1209  
 367 ValValProHisAsnGluCysSerGluValMetSerAsnMetValSerGluAsnMetLeu 386  
 1210 TGTGCGGCTACGACACCAAGCAGGAGGATCCCTGCCAGGGGACAGCGGGCGCGAC 1269  
 387 CysAlaGlyIleLeuGlyAspArgGlnAspAlaCysGluGlyAspSerGlyGlyProMet 406  
 1270 GTCACCCCTTCAAGGACACCTACTTCTGTCAGGACATCTGTCAGTGGGAGAGAGCTGT 1329  
 407 ValAlaSerPheHisGlyThrTrpPheLeuValGlyLeuValSerTrpGlyGluGlyCys 426  
 1330 GCCCGTAAGGGAACTACGAGTACACCAAGGTCACCGCTTCCTCAAGTGGATCGAC 1389  
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 1390 AGTGCTCATGAAACACAGGGGCTTGCCCAAGGCCAAGACCCATGCCCG 1437  
 447 GlyHisIleArgAspLysGluAlaProGln---LysSerTrpAlaPro 461

US-09-632-722-1 (1-1467) x US-09-978-917A-2 (1-461)

64 GAAAGTCTGTTCATCCGCGAGGAGGACCAACATCTCTGGCAGGCTCAGAGGCC 123  
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 124 AATTCCTCTTTTGAAGAGATGAAGAAAGACACCTCGAAAGAGATGTCATGAAAGAGACC 183  
 44 AsnSerPheLeuGluGluLeuArgHisSerSerLeuGluArgGluCysIleGluGlu 63  
 184 TGTCTATACAGAGACCGCGGAGTCTTTGAGGACAGCGACAGACGATGAATCTGG 243  
 64 CysAspPheGluGluAlaLysGluIlePheGlnAsnValAspThrLeuAlaPheTrp 83  
 244 AATAAATACAAAGATGGCAGCAGTGTGAGACGAGTCTT----- 282  
 84 SerLysHisValAspGlyAspGlnCysLeuValLeuProLeuHisProCysAlaSer 103  
 283 ---TGCAGACACGAGGCAATGTAAGACGCGCTCGGGAATATACACCTGACCTGTTTA 339  
 104 LeuCysCysGlyHisGlyThrCysIleAspGlyIleGlySerPheSerCysAspCysArg 123  
 340 GAGGATTCGAAGCAAACTGTGAATATTACACGAGGATC---TGCAGCTGGAC 396  
 124 SerGlyTrpGluGlyArgPheCysGlnArgGluValSerPheLeuAsnCysSerLeuAsp 143  
 397 AACGGGACGTGACCAAGTCTGCCACGAGGAGGTCAGTGTGCTGCTCCTCGCC 456  
 144 AsnGlyCysThrHisThrCysLeuGluValGlyTrpArgArgCysSerCysAla 163  
 457 CGCGGTGACCTGCTGACACGAGGAGGCTGATCCACAGCGGCTTCCACCGGCTTCCCTCT 516  
 164 ProGlyTyrLysLeuGlyAspAspLeuLeuGlnCysHisProAlaValLysPheProCys 183  
 517 GGGA---CAGACCTCGGACGAGGAGGTCAGTGTGCGCCAGCGCCACGACGAGC 570  
 184 GlyArgProTrpLysArgMetGluLysLysArgSerHisLeuLysArgAspThrGluAsp 203  
 571 AGCGGGGACCCCTGACACATCATGGAAGCCATATGATGACCGCGGAGCGCC 630  
 204 GlnGluAsp-----GlnValAspPro 210  
 631 ACCGAGAACCCTTCGACCTGCTGACTTCAACACGACGAGCTGAGAGGGCGGACAC 690  
 210 ----- 210  
 691 AACCTCACCAGATCGTGGGAGCGCAGGAATGCAAGGACGCGGAGTCTCCTCGCAGGCC 750  
 211 -----ArgIleIleAspGlyLysMetThrArgArgGlyAspSerProTrpGlnVal 227  
 751 CTGCTCATCAATAGGAAACGAGGGTTCTGTGTGGAACTATCTGACGCGATCTCTAC 810  
 228 ValLeuLeuAspSerLysLysLysLeuAlaCysGlyAlaValLeuIleHisProSerTrp 247  
 811 ATCTTAACGCGGACCTCTCTACCAAGCAAGATTCAGGTGAGGTGAGGAGGAC 870  
 248 ValLeuThrAlaAlaHisCysMetAspGlySerLysLeuValArgLeuGlyGlu 267  
 871 CGGAACACGAGGAGGAGGCGGTGACGCGGTGACGAGGTGGAGGTGGTCATCAAG 930  
 268 TyrAspLeuArgArgTrpGluLysTrpGluLeuAspLeuAspIleLysGluValPheVal 287





Db 232 SerThrTyrValProGlyThrThrAsnHisAspIleAlaLeuLeuArgLeuHisGlnPro 251  
 QY 994 ATCACTTCGCGTGAACGTGGCGCTGCTCCCTCCCGAGCGTGAAGTGGCGAGTCC 1053  
 Db 252 ValValLeuThrAspHisValValProLeuLeuCysLeuProGluArgThrPheSerGluArg 271  
 QY 054 ACGTGTATGACGACAGACGGGATGTGAGCGGCTTCGGGCGCCACCCACGAGAGAGGC 1113  
 Db 272 ThrLeuAlaPheValArgPheSerLeuValSerGlyTrpGlyGlnLeuLeuAspArgGly 291  
 QY 114 CGGCAGTCCACCGCTCAAGATGCTGGAGGTGCTCCCTACCTGACCGCCACACACTGC--- 1170  
 Db 292 AlaThrAlaLeuGluLeuMetValLeuAsnValProArgLeuMetThrGlnAspCysLeu 311  
 QY 171 -----AAGTGTCCAGCAGCTTCATCATCACCCAGCAACATGTTCTGTGCGGC 1218  
 Db 312 GlnGlnSerArgLysValGlyAspSerProAsnIleThrGlnThrMetPheCysAlaGly 331  
 QY 219 TACGACACCAAGCAGGAGGATGCTGCCAGGGGACAGCGGGCGCCGACGTCACCCGC 1278  
 Db 332 TyrSerAspGlySerLysAspSerCysLysGlyAspSerGlyGlyProHisAlaThrHis 351  
 QY 1279 TTCAAGCACACCTACTTCGTGACAGGATCGTCAGCTGGGGAGAGAGCTGTGCCCGTAAG 1338  
 Db 352 TyrArgGlyThrTrpThrLeuThrGlyIleValSerTrpGlyGlnGlyCysAlaThrVal 371  
 QY 339 GGGAGTACGGGATCTACACCAAGTCACCGCTTCCTCAAGTGGATCGACAGGTCATG 1398  
 Db 372 GlyHisPheGlyValTyrThrArgValSerGlnTrpIleGlnTrpLeuGlnLysLeuMet 391  
 QY 399 AAAACACGGGCTTGCCCAAGGCCAAGAGCCATGTCGCCCG 1437  
 Db 392 ArgSerGluProArgProGlyValValLeuLeuArgAlaPro 404

## RESULT 10

US-10-109-498-1

; Sequence 1, Application US/10109498

; Publication No. US20030044908A1

; GENERAL INFORMATION:

; APPLICANT: Persson, Egon

; TITLE OF INVENTION: Coagulation Factor VII Derivatives

; FILE REFERENCE: 6286.200-US

; CURRENT APPLICATION NUMBER: US/10/109,498

; CURRENT FILING DATE: 2002-03-22

; PRIORITY APPLICATION NUMBER: 60/281,261

; PRIORITY FILING DATE: 2001-04-03

; PRIORITY APPLICATION NUMBER: PA 2001 00477

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 406

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(406)

; OTHER INFORMATION: Xaa - Any Amino Acid

US-10-109-498-1

## Alignment Scores:

Pred. No.	Length:	Matches:
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Percent Similarity:	852.50	167
Best Local Similarity:	53.64%	76
Query Match:	36.87%	147
DB:	31.42%	63
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US-09-632-722-1 (1-1467) x US-10-109-498-1 (1-406)

QY 121 GCCAATTCCTTCTTGAAGAGATGAAGAAGGACACCTCGAAGAGAGTGCATGGAAGAG 180  
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QY 181 ACCTGCTCATACGAAGAGCGCCGAGGTCTTTGAGGACAGCGACAAGCAATCAATTC 240  
 Db 21 GlnCysSerPhe\*\*\*\*\*AlaArg\*\*\*IlePheLysAspAla\*\*\*ArgThrLysLeuPhe 40  
 QY 241 TCGAATAATACAAAGATGGCGACCATGTGTAGACAGTCTCTTGCAGAACACGAGGCAAA 300  
 Db 41 TrpIleSerTyrSerAspGlyAspGlnCysAlaSerSerProCysGlnAsnGlyLys 60  
 QY 301 TGTAAAGAGCGGCTCGGGGAATACACCTGCACCTGTTTGAAGAGTTCGAGAGCAAAAC 360  
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 Db 99 GluGlnTyrCysSerAspHisThrGlyThrLysArgSerCysArgCysHisGluGlyTyr 118  
 QY 466 ACCCTGGCTGACAAAGCGGCAAGCCCTGCATTCCACAGAGCCCTACCCCTGTGGGAAA--- 522  
 Db 119 SerLeuLeuAlaAspGlyValSerCysThrProThrValGluTyrProCysGlyLys 138  
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 Db 139 ProIleLeuGluLysArgAsnAlaSerLysProGlnGly----- 151  
 QY 583 CTTGACGATCATGGAAGCCATATGATGACGCCGACCTGGACCCACCCAGGAAACCCC 642  
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 QY 643 TTCGACCTGCTTGACTTCAACACAGCAGCAGCTGAGAGGGGGGAGCAACACTCACCAGG 702  
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 QY 823 GCCACTGCTCTACCAAGCAAGAGATTCAAG-----GTGAGGTAGGGAGCCGG 873  
 Db 192 AlaHisCysPheAspLysIleLysAsnTrpArgAsnLeuIleAlaValLeuGlyGluHis 211  
 QY 874 AACACGAGCAGGAGGCGGCGGTGAGCGGTGACAGAGTGTGGAGGTGTCTCATCAAGCAC 933  
 Db 212 AspLeuSerGluHisAspGlyAspGluGlnSerArgValAlaGlnValIleIlePro 231  
 QY 934 AACCGTTTCACAAAGGACACCTATGACTTCACATCCGCTGCTCCCGCTCAAGACCCCC 993  
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 QY 994 ATCACTTCCGATCAAGCTGGCGCTCTGCTCCCTCCCGAGCTGACTGGCGGAGTCC 1053  
 Db 252 ValValLeuThrAspHisValValProLeuCysLeuProGluArgThrPheSerGluArg 271  
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 Db 272 ThrLeuAlaPheValArgPheSerLeuValSerGlyTrpGlyGlnLeuLeuAspArgGly 291  
 QY 1114 CGGCAGTCCACCGCTCAAGATGCTGGAGGTGCTCCCTACCTGAGCCCGCCAGCAGTGC--- 1170  
 Db 292 AlaThrAlaLeuGluLeuMetValLeuAsnValProArgLeuMetThrGlnAspCysLeu 311  
 QY 1171 -----AAGTGTCCAGCAGCTTCATCATCACCCAGCAACATGTTCTGTGCGCGC 1218  
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Db      272 ThrLeuAlaPheValArgPheSerLeuValSerGlyTrpGlyGlnLeuLeuAspArgGly 291
QY      114 CGGCAGTCCACCGAGTCAAGATGCTGGAGGTGCTTACGTGGACCGCAACAGCTGC--- 1170
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QY      171 -----AAGTGTCACAGAGTTCATCATCACCCAGAACATGTTCTGTCGCCGC 1218
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QY      219 TAGCACCAACAGCAGGATGCTGCCAGGGGACAGGGGGCGCCGACGTCACCCGC 1278
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QY      339 GGAAGTACGGATCTACACCAAGTCCGCTCCCTCAAGTGGATCGACAGGTCCATG 1398
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## RESULT 9

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US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (16)
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; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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; LOCATION: (25)..(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

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; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

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## Alignment Scores:

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Pred. No.: 1,61e-46 Length: 406
Score: 852.50 Matches: 167
Percent Similarity: 53.64% Conservative: 76
Best Local Similarity: 36.87% Mismatches: 147
Query Match: 31.42% Indels: 63
DB: 11 Gaps: 8

US-09-632-722-1 (1-1467) x US-09-782-587B-1 (1-406)
QY 121 GCCAATTCCTTCTTGAAGAGATGAAGAAAGACACCTCGAAGAGAGTGCATGGAAGAG 180
Db 1 AlaAsnAlaPheLeu*****LeuArgProGlySerLeu***Arg***CysLys***** 20
QY 181 ACCTGCTCATACGAAGAGGCGCGAGGTCTTTGAGGACAGCAGCAAGACGAATTAATTC 240
Db 21 GlnCysSerPhe*****AlaArg**IlePheLysAspAla***ArgThrLysLeuPhe 40
QY 241 TGGATAAATAACAAGATGGCGACAGTGTGAGACCATCTCTTCCAGACAGCAAGGCAAA 300
Db 41 TrpIleSerTyrSerAspGlyAspGlnCysAlaSerSerProCysGlnAsnGlyCys 60
QY 301 TGTAAGACGGCGCTCGGGGAATACACCTGCACCTGTTTGTAGAGGATTCGAAGGCAAA 360
Db 61 CysLysAspGlnLeuGlnSerTyrIleCysPheCysLeuProAlaPheGluGlyArgAsn 80
QY 361 TGTGAATTAATTCACACAGGAAG-----CTCTGCAGCCTGGACAGCGGGAGCTGT 408
Db 81 CysGlu-----ThrHisLysAspGlnLeuIleCysValAsnGluAsnGlyCys 98
QY 409 GACCAAGTCTGCCAGCAGCAAGACAGACTCTGTG---GTGTCTCTCTGCGCCGCGGTAC 465
Db 99 GluGlnTyrCysSerAspHisThrGlyThrLysArgSerCysArgCysHisGluGlyTyr 118
QY 466 ACCCTGGCTGACACAGCGCAAGCCTGCATTCACAGCGCCCTACCCCTGTGGGAAA--- 522
Db 119 SerLeuLeuAlaAspGlyValSerCysThrProThrValGluTyrProCysGlyLysIle 138
QY 523 CAGACCTTGGAAACGACGAGGAGTCACTGTCAGTGGCCAGCCAGCAGCAGCGGGAGGCC 582
Db 139 ProIleLeuGluLysArgAsnAlaSerLysProGlnGly----- 151
QY 583 CCTGACAGCATCACATGGAAGCCATATGATGACGCCGACCTGGACCCCGACCGAACCC 642
Db 151 ----- 151
QY 643 TTCGACCTGCTTACTTCAACACAGACGAGCCTGAGAGGGCGGCAACAACCTCACAGG 702
Db 152 -----Arg 152
QY 703 ATCTGTGGAGCGCCAGGAATGAAGACGCGGGAGTGTCCCTGGCAGGCCCTGCTCATCAAT 762
Db 153 IleValGlyGlyLysValCysProLysGlyGluCysProTrpGlnValLeuLeuLeu--- 171
QY 763 GAGGAAAACGAGGGTTTCTGTGGTGAACATATCTTGACGCGAGTCTTACATCCTAACGCA 822
Db 172 ValAsnGlyAlaGlnLeuCysGlyGlyThrLeuIleAsnThrIleTrpValValSerAla 191
QY 823 GCCCACTGCTCTACCAAGCCCAAGAGATCAAG-----GTGAGGGTAGGGACCGG 873
Db 192 AlaHisCysPheAspLysIleLysAsnTrpArgAsnLeuIleAlaValLeuGlyLys 211
QY 874 ACACGGACGAGGAGGGCGGTGAGCGGTGACGAGGTGAGGTGAGGTGAGGTGAGGTGAG 933
Db 212 AspLeuSerGluHisAspGlyAspGlnSerArgValAlaGlnValIleIlePro 231
QY 934 AACCGGTTTCACAAAGGAGACCTATGACTTCGACATCGCGCTCGCGCTCAAGACCC 993
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233 AsnGlyAlaGlnLeuCysGlyGlyThrLeuIleAsnThrIleTrpValValSerAlaAla 252
    |||||||
826 CACTGTCTCTACCAAGCCAGAGATTCAAG-----GTGAGGTAGGGAGCCGGAAC 876
    |||||
253 HisCysPheAspLysIleLysAsnTrpArgAsnLeuIleAlaValLeuGlyGluHisAsp 272
    |||||
877 ACGGAGCAGGAGGAGCGGTGAGCGGTGCACGAGGTGGGTGCATCAAGCACAAC 936
    |||||
273 LeuSerGluHisAspGlyAspGluGlnSerArgValAlaGlnValIleIleProSer 292
    |||||
937 CGGTTCAAAAGGAGACTATGACTTCGACATCGCGCTGCTCGGCTCAAGACCCCATC 996
    |||||
293 ThrTyrValProGlyThrThrAsnHisAspIleAlaLeuLeuArgLeuHisGlnProVal 312
    |||||
997 ACCTTCGCGATGAACGTGGCGCTGCTGCTCCCGAGGTGACTGGCGCGAGTCCACG 1056
    |||||
313 ValLeuThrAspHisValValProLeuCysLeuProGluArgThrPheSerGluArgThr 332
    |||||
1057 CTGATGACGCGAAGACGGGATTTGTAGCGGCTTCGGGCGCCACCCACAGAGGGCCGG 1116
    |||||
333 LeuAlaPheValArgPheSerLeuValSerGlyTrpGlyGlnLeuLeuAspArgGlyAla 352
    |||||
117 CAGTCCACCGAGCTCAGATGCTGAGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1170
    |||||
353 ThrAlaLeuGluLeuMetValLeuAsnValProArgLeuMetThrGlnAspCysLeuGln 372
    |||||
171 -----AAGCTGTCCAGCAGCTTCATCATCACCAGAACATGTTCTGCGCGCTAC 1221
    |||||
373 GlnSerArgLysValGlyAspSerProAsnIleThrGluTrpMetPheCysAlaGlyTyr 392
    |||||
222 GACACCAAGCAGGAGGATGCTGCCAGGGGACAGCGGGCGCCCGCCAGCTCACCGCTTC 1281
    |||||
393 SerAspGlySerLysAspSerCysLysGlyAspSerGlyGlyProHisAlaThrHisTyr 412
    |||||
282 AAGCACACTACTCTGTGACAGCATCGTACGTGGGAGAGAGTGTGCTCCCTAAGGG 1341
    |||||
413 ArgGlyThrTrpTrpTrpGlyIleValSerTrpGlyGlnGlyCysAlaThrValGly 432
    |||||
342 AAGTACGGATCTACACCAAGTCAACCGCTTCTCAAGTGGATGCACAGGTCCATGAA 1401
    |||||
433 HisPheGlyValTyrThrArgValSerGlnTyrIleGluTrpLeuGlnLysLeuMetArg 452
    |||||
402 ACCAGGGCTGCGCCAGGCCACAGCCATGCGCCCG 1437
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453 SerGluProArgProGlyValLeuLeuArgAlaPro 464

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## RESULT 8

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US-09-782-3 587B-3
; Sequence 3, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VITA-LIKE MOLECULES
; FILE REFERENCE: 31-001000S
; CURRENT FILING DATE: 2002-03-26
; PRIORITY FILING DATE: 2002-03-26
; PRIORITY FILING DATE: 2000-02-11
; PRIORITY FILING DATE: 2000-02-11
; PRIORITY FILING DATE: 2000-02-22
; PRIORITY FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-782-3 587B-3

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## Alignment Scores:

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Pred. No.: 3,74e-50 Length: 406
Score: 909.50 Matches: 176
Percent Similarity: 55.85% Conservative: 77
Best Local Similarity: 38.85% Mismatches: 137
Query Match: 33.52% Indels: 63
DB: 11 Gaps: 8

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US-09-632-722-1 (1-1467) x US-09-782-587B-3 (1-406)

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QY 121 GCCAATTCCTTTCTTGAAGAGATGAAGAAAGACACCTCGAAGAGAGAGTGCATGGAAG 180
    |||||||
Db 1 AlaAsnAlaPheLeuGluGluLeuArgProGlySerLeuGluArgGluCysLysGluGlu 20
    |||||||
QY 181 ACCTGCTCATACGAAGAGCGCCGCGAGGTCTTTGAGGACAGCAGCAGCAAGCAATGATC 240
    |||||||
Db 21 GlnCysSerPheGluGluAlaArgGluIlePheLysAspAlaGluArgThrLysLeuPhe 40
    |||||||
QY 241 TGAATATAATACAAAGATGGCAGCAGTGTGAGACAGTCTTGCAGAACACAGGGCAAA 300
    |||||
Db 41 TrpIleSerTyrSerAspGlyAspGlnCysAlaSerSerProCysGlnAsnGlyGlySer 60
    |||||||
QY 301 TGTAAAGACGGCTCGGGGAATACACCTGCACCTGTTTAGAAGAGTTCGAAGGCAAAAC 360
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Db 61 CysLysAspGlnLeuGlnSerTyrIleCysPheCysLeuProAlaPheGluGlyArgAsn 80
    |||||||
QY 361 TGTGAATATTACACACGGAG-----CTCTGCAGCCTGCAGAACAGGGGACTGT 408
    |||||||
Db 81 CysGlu-----ThrHisLysAspAspGlnLeuIleCysValAsnGluAsnGlyGlyCys 98
    |||||||
QY 409 GACCAAGTCTGCGACGAGGAGAACAGAACTCTGTG-----GTGTGCTCTCGCGCCGCGGTAC 465
    |||||||
Db 99 GluGlnTyrCysSerAspHisThrGlyThrLysArgSerCysArgCysHisGluGlyTyr 118
    |||||||
QY 466 ACCCTGGTGAACAGCGACCGCTGCATTCCTCCAGCGGCCCTACCTCTGTGGGAAA--- 522
    |||||||
Db 119 SerLeuLeuAlaAspGlyValSerCysThrProThrValGluTyrProCysGlyLysIle 138
    |||||||
QY 523 CAGACCTTGAACGACGAGGAGGTGAGTGGCGCCAGCCACCAGCAGCAGCGGGGAGGCC 582
    |||||||
Db 139 ProIleLeuGluLysArgAsnAlaSerLysProGlnGly----- 151
    |||||||
QY 583 CCGTACAGCATCACATGGAAGCCATATGATGACGCCGACCTGGAGCCGCCAGAGAACCCC 642
    |||||||
Db 151 ----- 151
    |||||||
QY 643 TTCGACCTGCTTGACTTCAACCAGCAGCGCTGAGAGGGGGGAGCAACACTCACAGG 702
    |||||||
Db 152 -----Arg 152
    |||||||
QY 703 ATCGTGGGAGCGCAGGAATGCAAGACGGGAGTGTCTCGCAGCGCCCTGCTCATCAAT 762
    |||||||
Db 153 IleValGlyGlyLysValCysProLysGlyGluCysProTrpGlnValLeuLeuLeu--- 171
    |||||||
QY 763 GAGGAAAACGAGGGTTTCTGTGGTGAACATTTCTGACGAGTGTTCATCATCTCAACGCA 822
    |||||||
Db 172 ValAsnGlyAlaGlnLeuCysGlyGlyThrLeuIleAsnThrIleTrpValValSerAla 191
    |||||||
QY 823 GCCCACTGCTCTACCAAGCCCAAGAGATTCAAG-----GTGAGGTAGGGAGCGG 873
    |||||||
Db 192 AlaHisCysPheAspLysIleLysAsnTrpArgAsnLeuIleAlaValLeuGlyGluHis 211
    |||||||
QY 874 AACACGGAGCAGGAGGGCGGTGAGCGGTGCACGAGGTGGGTGCTCATCAAGCAC 933
    |||||||
Db 212 AspLeuSerGluHisAspGlyAspGluGlnSerArgValAlaGlnValIleIlePro 231
    |||||||
QY 934 AACCGGTTCAAAAGAGAGACCTATGACTTCGACATCGCGCTCGCGCTCAAGACCCCC 993
    |||||||
Db 232 SerThrTyrValProGlyThrThrAsnHisAspIleAlaLeuLeuLeuLeuHisGlnPro 251
    |||||||
QY 994 ATCACCITTCGCGATGAACGTGGCGCTGCTCGCTCCCGGAGCGTGACTGGCGCGAGTCC 1053
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550 GTGGCCAGGCGCCAGCAGCAGCGGGAGGCGCCCTGACAGCATCATGGAAGCCATAT 609
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140 ThrSerLysLeuThrArgAlaGluThrValPheProAsp-----Val 153
      ::::: ||| ::| |||||
610 GATGACGCGGACTGGACCCCGACCGAGAACCCCTTCGACCTGCTTGAATTCACACAGACG 669
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154 AspTyrValAsnSerThrGluAlaGluThrIleLeuAsp-----AsnIleThr 169
      ::::: ||| ::| |||||
670 CAGCCTGACAGGGCGGCACACACACCTCACCAGGATCGTGGAGCCAGGAATGCAAGGAC 729
      ||| ::| |||
170 GlnSerThrGlnSerPheAsnAspPheThrArgValValGlyGluAspAlaLysPro 189
      ::::: ||| ::| |||||
730 GGGGAGTGTCCCTGGCAGGCGCTGCTCATCAATGAGGAAACGAGGGTTCTGTGCTGGA 789
      ||| ::| |||
190 GlyGlnPheProTyrPheValValLeu---AsnGlyLysValAspAlaPheCysGlyGly 208
      ::::: ||| ::| |||||
790 ACTATTCTGAGGAGTTTACATCTTAAGCGGCCCTACTGCTTACCAAGCCAAAGAGA 849
      ::::: ||| ::| |||||
209 SerIleValAsnGluLysTrpIleValThrAlaAlaHisCysValGluThrGlyValLys 228
      ::::: ||| ::| |||||
850 TTCAGGTGAGGTAGGCGACCGGACACGCGGAGCAGGAGGCGGCTGAGCGGCTGCAC 909
      ||| ::| |||
229 IleThrValValAlaGlyGluHisAsnIleGluGluThrGluHisThrGluGlnLysArg 248
      ::::: ||| ::| |||||
910 GAGGTGAGGTGCTCATCAAGCACACACCGGTTTCAACAAG-----GAGACCTATGACTTC 963
      ||| ::| |||
249 AsnValIleArgIleIleProHisHisAsnTyrAsnAlaAlaIleAsnLysTyrAsnHis 268
      ::::: ||| ::| |||||
964 GACATCGCGGTGCTCGGCTCAAGACCCCATCCTCCCGATGAACTGCGGCTGCC 1023
      ||| ::| |||
269 AspIleAlaLeuLeuGluLeuAspGluProLeuValLeuAsnSerTyrValThrProIle 288
      ::::: ||| ::| |||||
024 TGCTCCCGCGGTGCTGCGGCGGAGTCCAGCTGATGACGACGAGACGCGGATTTGG 1083
      ||| ::| |||
289 CysIleAlaAspLysGluTyrThr---AsnIlePheLeuLysPheCysGlyTyrVal 307
      ::::: ||| ::| |||||
084 AGCGGCTTCGGGCGCACCCAGCAGAGAGGCGCGGCTCCAGCTCCAGGCTCAAGATGCTGGAG 1143
      ||| ::| |||
308 SerGlyTrpGlyArgValPheHisLysGlyArgSerAlaLeuValLeuGlnTyrLeuArg 327
      ::::: ||| ::| |||||
144 GTGCCCTAGTGGACCGGACAGCTGCAAGCTGTCAGCAGCTTTCATCATCACCAGAAC 1203
      ||| ::| |||
328 ValProLeuValAspArgAlaThrCysLeuAlaSerThrLysPheThrIleTyrAsnAsn 347
      ::::: ||| ::| |||||
204 ATGTTCTGTCCGGCTACGACACCAAGCAGGAGGATGCTCCAGGGGACAGCGGGGCG 1263
      ||| ::| |||
348 MetPheCysAlaGlyPheHisGluGlyGlyArgAspSerCysGlnGlyAspSerGlyGly 367
      ::::: ||| ::| |||||
264 CGCAGCTCACCGGCTTCAAGGACACCTACTTCTGTGACAGGATCGTCAGCTGGGGAGAG 1323
      ||| ::| |||
368 ProHisValThrGluValGluGlyThrSerPheLeuThrGlyIleIleSerTrpGlyGlu 387
      ::::: ||| ::| |||||
324 AGCTGTCCCGTAAAGGAGTACGGATCTACACCAAGTCCACCGCTTCTCCTCAAGTGG 1383
      ||| ::| |||
388 GluCysAlaMetLysGlyLysTyrGlyIleTyrThrLysValSerArgTyrValAsnTrp 407
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384 ATCGACAGGTCCCATGAAA 1401
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408 IleLysGluLysThrLys 413
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RESULT 7

US-10-017

2, Application US/10017122

Publication No. US20030087244A1

GENERAL

INFORMATION:

APPLICANT: McCarthy, Jeanette

FILE REFERENCE: MMI-007

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE

CURRENT APPLICATION NUMBER: US/10/017,122

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/327,487

PRIOR FILING DATE: 2001-10-09

NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 466

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-017-122-2

Alignment Scores:

Pred. No.:	1,34e-52	Length:	466
Score:	948.00	Matches:	189
Percent Similarity:	53.71%	Conservative:	86
Best Local Similarity:	36.91%	Mismatches:	155
Query Match:	34.94%	Indels:	82
DB:	15	Gaps:	9

US-09-632-722-1 (1-1467) x US-10-017-122-2 (1-466)

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QY 1 ATGGGGGCGCCATGCGACCTGCTGCTCCTAGTCCCTCCCTGGTGGCTGCTGCTGCTGCTC 60
DB 2 ValSerGlnAlaLeuArgLeuLeuCysLeuLeuGlyLeuGlnGlyCysLeuAlaAla 21
      ::::: ||| ::| |||||
QY 61 GGG----- 63
DB 22 GlyGlyValAlaLysAlaSerGlyGlyGluThrArgAspMetProTyrLysProGlyPro 41
      |||
QY 64 GAAAGTGTGTTTCATCCGCGAGGAGCGCCCAACCAACATCTGGCGAGGGTCCACGAGGCC 123
      ::::: ||| ::| |||||
DB 42 HisArgValPheValThrGlnGluGluAlaHisGlyValLeuHisArgArgAla 61
      ::::: ||| ::| |||||
QY 124 AATTCCTTCTTGAAGAGATGAAGAAGGACACCTCCAAAGAGAGTGCATGGAAGAGACC 183
      ::::: ||| ::| |||||
DB 62 AsnAlaPheLeuGluLeuArgProGlySerLeuGluArgGluCysLysGluGluGln 81
      ::::: ||| ::| |||||
QY 184 TGCTCATACGAGAGCGCGGAGGTCTTTGAGCAGCAGCGACAAGCAATGAATTCGTGG 243
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DB 82 CysSerPheGluGluAlaArgGluIlePheLysAspAlaGluArgThrLysLeuPheTrp 101
      ::::: ||| ::| |||||
QY 244 AATAAATAAAGATGGCGACCATGCTGTGAGCAGTCTCTCCAGAACACGAGGCAATGT 303
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DB 102 IleSerTyrSerAspGlyAspGlnCysAlaSerProCysGlnAsnGlyGlySerCys 121
      ::::: ||| ::| |||||
QY 304 AAAGACGCGCTCGGGATACACCTGCGACCTGTTTAGAAGATTCGAGGCAAAACTGT 363
      ::::: ||| ::| |||||
DB 122 LysAspGlnLeuGlnSerTyrIleCysPheCysLeuProAlaPheGluGlyArgAsnCys 141
      ::::: ||| ::| |||||
QY 364 GAATTAATTCACACGGAAG-----CTCTGACGCTGGACACAGCGGAGCTGTGAC 411
      ::::: ||| ::| |||||
DB 142 Glu-----ThrHisLysAspGlnLeuIleCysValAsnGluGlyCysGlu 159
      ::::: ||| ::| |||||
QY 412 CAGTTCTGCCAGGAACAGAACTCTGTG---GTGTGCTCCTGGCGCGGGGTACACC 468
      ::::: ||| ::| |||||
DB 160 GlnTyrCysSerAspHisThrGlyThrLysArgSerCysArgCysHisGluGlyTyrSer 179
      ::::: ||| ::| |||||
QY 469 CTGGCTGACACGCGCAAGCGCTGCATTCACAGGCGCTTACCCTGTGGGAAA---CAG 525
      ::::: ||| ::| |||||
DB 180 LeuLeuAlaAspGlyValSerCysPheCysLeuProThrValGlnTyrProCysGlyLysIlePro 199
      ::::: ||| ::| |||||
QY 526 ACCCTGGAACGACGAGAGAGTGTGCTGCGCCAGCGCCACACGACGAGCGGGAGGCCCT 585
      ::::: ||| ::| |||||
DB 200 IleLeuGluLysArgAsnAlaSerLysProGlnGly----- 211
      ::::: ||| ::| |||||
QY 586 GACAGCATCATGGAAGCCATATGATGACCGCGACCTGGACCCACCGAGAACCCCTTC 645
      ::::: ||| ::| |||||
DB 211 ----- 211
      ::::: ||| ::| |||||
QY 646 GACCTGCTTGAATCAACACGACGAGCCTGAGAGGGGCGACAAACCTCACCAGGATC 705
      ::::: ||| ::| |||||
DB 212 -----ArgIle 213
      ::::: ||| ::| |||||
QY 706 GTGGGAGCGCCAGGAATGCAAGACGCGGAGTGTCCCTGGCAGGCGCTGCTCATCAAGAG 765
      ::::: ||| ::| |||||
DB 214 ValGlyGlyLysValCysProLysGlyGluCysProTyrGlnValLeuLeuLeu---Val 232
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Db 54 GluPheValGlnGlyAsnLeuGluArgGluCysMetGluGluLysCysSerPheGluGlu 73  
QY 199 GCCCGAGGTCCTTTAGGAGCAGCACAAGCAAGTAATCTGGAATAAATCAAGAT 258  
Db 74 AlaArgGluValPheGluAsnThrGluArgThrGluPheTrpLysGlnTrpValAsp 93  
QY 259 GCGCACCAGTGTGAGACCACTCCTTCCAGAACAGGCAAAATGTAAAGACGCCCTCGG 318  
Db 94 GlyAspGlnCysGluSerAsnProCysLeuAsnGlyCysSerCysLysAspAspIleAsn 113  
QY 319 GAATACACCTGCACCTCTTTAGAGGATTCGAAGGCAAAACACTGTAATTAATTCACACG 378  
Db 114 SerTyrGluCysTrpCysPropheGlyPheGluGlyLysAsnCysGluLeuAspVal--- 132  
QY 379 AAGCTCTGACCTGGCAACAGCGGACTGTGACCACTTCTGC---CACGAGGAACAAC 435  
Db 133 ---ThrCysAsnIleLysAsnGlyArgCysGluGlnPheCysLysAsnSerAlaAspAsn 151  
QY 436 TCTGTGTGTGTCCTCGCCCGCGGTACACCTCGGTGACACAGCGCAAGCGCTGCATT 495  
Db 152 LysValValCysSerCysThrGluGlyTyrArgLeuAlaGluAsnGlnLysSerCysGlu 171  
QY 496 CCCAGGCGCCCTACCCCTGTGGGAAACAGACAGCCTCGAAGAGGTCAGTGGCC 555  
Db 172 ProAlaValProPheProCysGlyArgValSerValSerGln-----ThrSer 187  
QY 556 CAGGCCACAGCAGCAGCGGGAGGCCCTGACAGCATCATGGAAGCCATATGATGCA 615  
Db 188 LysLeuThrArgAlaGluThrValPheProAsp-----ValAspTyr 201  
QY 616 GCGCAGCTGGACCCCGAGCAACCCCTTCGACCTCTGACTTCAACAGCAGCGACCT 675  
Db 202 ValAsnSerThrGluAlaGluThrIleLeuAsp-----AsnIleThrGlnSer 217  
QY 676 GAGAGGGGCGCAACACCTCCAGGATCGTGGGAGCGCAAGATGCAAGACGGGAG 735  
Db 218 ThrGlnSerPheAsnAspPheThrArgValValGlyGluAspAlaLysProGlyGln 237  
QY 736 TGTCCCTGCGAGCCCTGCTCATCATGATGAGAAACAGCGGTTCTGTGGTGGCACTATT 795  
Db 238 PheProTrpGlnValValLeu---AsnGlyLysValAspAlaPheCysGlyGlySerIle 256  
QY 796 CTGAGCGAGTTCATCTTAACGCGAGCCGCTGCTCTACCAAGCCCAAGATTCAG 855  
Db 257 ValAsnGluLysTrpIleValThrAlaAlaHisCysValGluThrGlyValLysIleThr 276  
QY 856 GTGAGGTAGGGACCGGACAGCAGGAGGAGGCGGCGGTGAGCGGTGCACAGGTG 915  
Db 277 ValValAlaGlyGluHisAsnIleGluGluThrGluHisThrGluGlnLysArgAsnVal 296  
QY 916 GAGGTGCTCATCAAGCACACCGGTTCAACAAG-----GAGACCTATGACTTCGACATC 969  
Db 297 IleArgIleIleProHisHisAsnTyrAsnAlaAlaIleAsnLysTyrAsnHisAspIle 316  
QY 970 GCGGTCTCGGCTCAAGACCCCATCATCTCCGATGAAAGTGGCGGCTCGCTGCCTC 1029  
Db 317 AlaLeuLeuGluLeuAspGluProLeuValLeuAsnSerTyrValThrProIleCysIle 336  
QY 1030 CCGGACGCTGACTGGGCGGAGTCCAGCTGATGACGACAGACGGGATGTCAGCGGC 1089  
Db 337 AlaAspLysGluTrpThr---AsnIlePheLeuLysPheGlySerGlyTyrValSerGly 355  
QY 090 TTCGGGCGCCACCGAGAGGCGGAGTCCACGAGCTCAAGATGCTGGAGTGCC 1149  
Db 356 TrpGlyArgValPheHisLysGlyArgSerAlaLeuValLeuGlnTrpValPro 375  
QY 150 TACGTGGCCGCAACAGCTGCAAGCTGTCCAGCACTTCATCATCACCCAGAAATGTC 1209  
Db 376 LeuValAspArgAlaThrCysLeuArgSerThrLysPheThrIleTyrAsnAsnMetPhe 395  
QY 210 TGTGCGGCTACGACACCAAGCAGGAGGATGCTCCAGGAGGAGCGGCGGCGCCGAC 1269  
Db 396 CysAlaGlyPheHisGluGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProHis 415

QY 1270 GTCAACCCGCTTCAAGACACACCTACTCTGTGACAGGCATCTGTCAGCTGGGGAGAGAGCTGT 1329  
Db 416 ValThrGluValGluGlyThrSerPheLeuThrGlyIleIleSerTrpGlyGluGluCys 435  
QY 1330 GCCCTTAAGGGAGAGTACGGGATCTACACCAAGGTACCGCTCTCTCAAGTGGATCGAC 1389  
Db 436 AlaMetLysGlyLysTyrGlyIleThrLysValSerArgTyrValAsnTrpIleLys 455  
QY 1390 AGTCCATGAAA 1401  
Db 456 GluLysThrLys 459

## RESULT 6

US-09-118-748-2  
; Sequence 2, Application US/09118748A  
; Patent No. US20020031799A1  
; GENERAL INFORMATION:  
; APPLICANT: Stafford, Darrel W.  
; APPLICANT: Chang, Jinli  
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting  
; FILE REFERENCE: 5470-183  
; CURRENT APPLICATION NUMBER: US/09/118,748A  
; CURRENT FILING DATE: 1998-07-17  
; EARLIER APPLICATION NUMBER: 60/053,571  
; EARLIER FILING DATE: 1997-07-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-118-748-2

Alignment Scores:  
Pred. No.: 1,07e-55 Length: 415  
Score: 996.50 Matches: 192  
Percent Similarity: 61.74% Conservative: 71  
Best Local Similarity: 45.07% Mismatches: 142  
Query Match: 36.73% Indels: 21  
DB: Gaps: 9

US-09-632-722-1 (1-1467) x US-09-118-748-2 (1-415)  
QY 133 CTTGAAGAGATGAAGAAGACACCTCGAAGAGAGTGCATGGAAGAGACCTGCTCATAC 192  
Db 6 LeuGluGluPheValGlnGlyAsnLeuGluArgGluCysMetGluGluLysCysSerPhe 25  
QY 193 GAAGAGCCCGGAGGCTTTTGAGCAGCAGCGACAGCAGAGTGAATCTCGAATAATAC 252  
Db 26 GluGluAlaArgGluValPheGluAsnThrGluArgThrThrGluPheTrpLysGlnTyr 45  
QY 253 AAAGATGGCAGCACAGTGTGAGACAGCTTCCAGAACAGCGGCAAAATGTAAGAGCGGC 312  
Db 46 ValAspGlyAspGlnCysGluSerAsnProCysLeuAsnGlyGlySerCysLysAspAsp 65  
QY 313 CTCGGGGAATACACCTGCACCTGTTTGAAGAGTTCGAAGCAAAACTGTGAATTATTC 372  
Db 66 IleAsnSerTyrGluCysTrpCysPropheGlyPheGluGlyLysAsnCysGluLeuAsp 85  
QY 373 ACAGGAGCTCTGCACCTGGACAGCGGAGCTGTGACCACTTCTGC---CACGAGGAA 429  
Db 86 Val-----ThrCysAsnIleLysAsnGlyArgCysGluGlnPheCysLysAsnSerAla 103  
QY 430 CAGACACTCTGTGGTGTCTCTCGCCCGCGGTACACCTGCTGACACGACGCAAGGCC 489  
Db 104 AspAsnLysValValCysSerCysThrGluGlyTyrArgLeuAlaGluAsnGlnLysSer 123  
QY 490 TGCATTCCCAAGGCGCCTTACCCCTGTGGGAAACAGACCTGGAAGCAGGAGAGGTCA 549  
Db 124 CysGluProAlaValProPheProCysGlyArgValSerValSerGln----- 139

14 LeuileThrIleCysLeuLeuGlyTyrLeuLeuSerAlaGluCysThrValPheLeuAsp 33  
 82 AGGAGCAGGCGCAACAATCTCTGGGAGGTCACGAGGCCAATTC---TTTCTTGAA 138  
 34 HisGluAsnAlaAsnLysIleLeuAsnArgProLysArgTyrAsnSerGlyLysLeuGlu 53  
 139 GAGATGAAGAAGGACACCTCTGAAGAGAGTGTGATGAAGAGACCTCTCATACGAAGAG 198  
 54 GluPheValGlnGlyAsnLeuGluArgGluCysMetGluGluLysCysSerPheGluGlu 73  
 199 GCCCGCAGGCTTTTGGAGCAGCAGCAAGCAAGCAAGTTCGGAATTAATACAAAGAT 258  
 74 AlaArgGluValPheGluAsnThrGluArgThrThrGluPheTrpLysGlnTyrValAsp 93  
 259 GCGCAGCAGTGTGACACAGCTCTTGCACAGCAGGCAAGCAAGTAAAGACGCCCTCGG 318  
 94 GlyAspGlnCysGluSerProCysLeuAsnGlyGlySerCysLysAspIleAsn 113  
 319 GAATACACCTGCACCTGTTTGAAGAGTTCGAAGGCAAAACTGTGAATTTATCACACGG 378  
 114 SerTyrGluCysTrpCysProPheGlyPheGluGlyLysAsnCysGluLeuAspVal--- 132  
 379 AGCTCTGCAGCTGGCAACAGGAGCTGTACACAGTTCG---CACGAGGACAGAAC 435  
 133 ---ThrCysAsnIleLysAsnGlyArgCysGluGlnPheCysLysAsnSerAlaAspAsn 151  
 436 TCTGTGGTGTCTCTGCGCGCGGGGTACACCTGTGACACGCGCAAGCGCTCATTT 495  
 152 LysValValCysSerCysThrGluGlyTyrArgLeuAlaGluAsnGlnLysSerCysGlu 171  
 496 CCCACAGGCGCTACCTGTGGGAACAGACCTGTGAACCGCAGGAGAGTTCAGTGGCC 555  
 172 ProAlaValProPheProCysGlyArgValSerGln-----ThrSer 187  
 556 CAGGCGCACAGCAGGCGGGGCGCCCTGCACAGCATCATGGAAGCCATGATGCA 615  
 188 LysLeuThrArgAlaGluThrValPheProAsp-----ValAspTyr 201  
 616 GCGCAGCTGGACCCACAGCAGAACCCCTTCGACCTGTGACTTCAACAGCAGCAGCT 675  
 202 ValAsnSerThrGluAlaGluThrIleLeuAsp-----AsnIleThrGlnSer 217  
 676 GAGAGGGGCGACAACTCACCAGGATCTGGGAGGCGCAGGAATCGAAGCGGGAG 735  
 218 ThrGlnSerPheAsnAspPheThrArgValValGlyGlyGluAspAlaLysProGlyGln 237  
 736 TGTCTCTGCGAGCGCTCTCATCAATCAGGAAACAGAGGTTTCTGTGTGGAATATT 795  
 238 PheProTrpGlnValValLeu---AsnGlyLysValAspAlaPheCysGlyGlySerIle 256  
 796 CTGAGCGAGTTCTACATCTACGCGCGCCCTCTCTCTACCAAGCAAGAGATTCAAG 855  
 257 ValAsnGluTyrTrpIleValThrAlaAlaHisCysValGluThrGlyValLysIleThr 276  
 856 GTGAGGAGTGGGCGGCAACACGAGGAGGCGGCTGAGCGGTCACAGAGGTG 915  
 277 ValValAlaGlyGluHisAsnIleGluGluThrGluHisThrGluGlnLysArgAsnVal 296  
 916 GAGTGTCTATCAGCAGCAACCGTTTCAAG-----GAGACCTATGACTTCGATC 969  
 297 IleArgIleIleProHisAsnTyrAsnAlaAlaIleAsnLysTyrAsnHisAspIle 316  
 970 GCGTGTCTCGGCTCAAGACCCCATCATCTTCGATGAACGTCGCGCTGCTCGCTC 1029  
 317 AlaLeuLeuGluLeuAspGluProLeuValLeuAsnSerTyrValThrProIleCysIle 336  
 030 CCGCAGCGTGTGCGGCGGTCACGTCATGACGAGAGAGCGGATTTGTGAGCGC 1089  
 337 AlaAspLysGluTyrThr---AsnIlePheLeuLysPheGlySerGlyTyrValSerGly 355  
 090 TTCGGCGCACCCACGAGAGGCGCGGCGAGTCCACAGGCTCAAGATGCTCGGAGTGGCC 1149





OPERATING SYSTEM: DOS  
SOFTWARE: FASTSQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/348,504  
FILING DATE: 29-Jan-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/367,777  
FILING DATE: 10-NO. US20030138914A1-1999  
APPLICATION NUMBER: AT A 336/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCr/At98/00046  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Aussenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 20695D-0009000US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>

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Alignment Scores:
Pred. No.      Length:      488
Score:         2634.00    Matches:      488
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%    Mismatches:  0
Query Match:   97.09%      Indels:       0
DB:            12          Gaps:         0

US-09-632722-1 (1-1467) x US-10-348-504-44 (1-488)

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1



# INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 306 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 59..64

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 79..95

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 160

OTHER INFORMATION: /note= "Disulfide linkage to

OTHER INFORMATION: residue 132 of SEQ ID NO:2"

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 208..222

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 233..261

FEATURE:

US-08-474-042-1

Alignment Scores:

Pred. No. 6.89e-121 Length: 306

Score: 1631.00 Matches: 305

Percent Similarity: 99.67% Conservative: 0

Best Local Similarity: 99.67% Mismatches: 1

Query Match: 60.12% Indels: 0

DB: 1 Gaps: 0

US-09-632-722-1 (1-1467) x US-08-474-042-1 (1-306)

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QY 547 TCAGTGGCCAGCCACCAGCAGCAGCGGGAGGCCCTGACAGCATCATCGGAAGCCA 606
DB 1 SerValAlaGlnAlaThrSerSerGlyGluAlaProAspSerIleThrTrpLysPro 20
QY 607 TATGATGCAGCGACCTGGACCCCGAGACCCCTTCGACCTGCTTCAACCCAG 666
DB 21 TyrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuAspPheAsnGln 40
QY 667 ACGCAGCCTGAGAGGGCGCACACACCTCACAGGATCGTGGAGGCCAGGAATGCCAG 726
DB 41 ThrGlnProGluArgGlyAspAsnLeuThrArgIleValGlyGlnGluCysLys 60
QY 727 GACGGGAGTGTCCCTGGCAGGCCCTGCTCATCAATGAGAAACGAGGGTTCTGTGT 786
DB 61 AspGlyGluCysProThrGlnAlaLeuLeuIleAsnGluAsnGluGlyPheCysGly 80
QY 787 GGAACTATTCTGAGCGAGTTCTACATCTTAACGGCAGCCACTGTCTTACCAAGCCAAG 846
DB 81 GlyThrIleLeuSerGluPheThrIleLeuThrAlaAlaHisCysLeuThrGlnAlaLys 100
QY 847 AGATTCAAGGTGAGGTAGGCGGACCGGACACGAGCAGGAGGCGGGTTCAGCGCGTG 906
DB 101 ArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlyGluAlaVal 120
QY 907 CACGAGGTGGAGTGGTTCATCAAGCACACCGGTTTCAAAAGGAGACCTATGACTTCGAC 966
DB 121 HisGluValGluValIleLysHisAsnArgPheThrLysGluThrTyrAspPheAsp 140
QY 967 ATCGCGCTGCTCCGCTCAAGACCCCATCACCCTTCGGGATGAGACGTGGCGCTGCCTGC 1026
DB 141 IleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaProAlaCys 160
QY 1027 CTCGCCGAGCGTACTGGCGCCAGTCCACGCTGATGACGACAGACGCGGATTCGTGAC 1086
DB 161 LeuProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyIleValSer 180
QY 087 GCCTTCGGCGGCACCCACGAGAGGGCGGCGAGTCCACAGGCTCAAGATGCTGGAGGTG 1146

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Search completed: August 11, 2003, 10:51:13  
Job time : 52.5 secs

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DB 181 GlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeuGluVal 200
QY 1147 CCCTACGTGGACCGCAACAGCTGCAAGCTGCCAGAGCTTCATCATCATCACCAGAACATG 1206
DB 201 ProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGlnAsnMet 220
QY 1207 TTCTGTCCGGCTACGACACCAAGCAGGAGGATGCTGCCAGGGGACAGCGGGGCCCG 1266
DB 221 PheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGlyGlyPro 240
QY 1267 CACGTACCCCGCTTCAAGGACACCTTCTGTCAGGACATCGTCAGCTGGGGAGAGAGC 1326
DB 241 HisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGlyGluGly 260
QY 1327 TGTGCCCGTAAGGGAGTACGGGATCTACACCAAGTTCACCGCTTCCCTCAAGTGGATC 1386
DB 261 CysAlaArgLysGlyLysTyrGlyIleThrLysValThrAlaPheLeuLysTrpIle 280
QY 1387 GACAGGTCCATGAAACACAGGGGCTTGCCCAAGGCCAAGAGCCATGCCCGGAGGTGATA 1446
DB 281 AspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGluValIle 300
QY 1447 ACGTCTCTCCATTAAG 1464
DB 301 ThrSerSerProLeuLys 306

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;; PRIOR APPLICATION DATA:  
 ;; APPLICATION NUMBER: US 08/484,558  
 ;; FILING DATE: 07-JUN-1995  
 ;; ATTORNEY/AGENT INFORMATION:  
 ;; NAME: Murashige, Kate H.  
 ;; REGISTRATION NUMBER: 29,959  
 ;; REFERENCE/DOCKET NUMBER: 2803-0007.02  
 ;; TELEPHONE: (202)887-1500  
 ;; TELEFAX: (202)822-0168  
 ;; TELE: 90-4030 MRSNFOERSWSH  
 ;; INFORMATION FOR SEQ ID NO: 1:  
 ;; SEQUENCE CHARACTERISTICS:  
 ;; LENGTH: 306 amino acids  
 ;; TYPE: amino acid  
 ;; STANDARDS: single  
 ;; TOPOLOGY: linear  
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QY 967 ATCCGCGTCTCCGGCTCAAGACCCCATCACCTTCGATGACGTGGCGCTGCTGC 1026  
 Db 141 IleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaProAlaCys 160  
 QY 1027 CTCCCGAGCGTGACTGGCGGAGTCCACGCTGATGACGAGAGAGCGGGATTGTGAGC 1086  
 Db 161 LeuProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyIleValSer 180  
 QY 1087 GGCTTCGGGCGCACCCAGGAGGCGGCGGAGTCCACCGAGTCCACCGAGTCCAGAGTGTGAGGTG 1146  
 Db 181 GlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeuGluVal 200  
 QY 1147 CCCTACGTGGACCGCAACAGCTGCAAGCTGTCCAGCAGCTTCATCATCACCAGAACATG 1206  
 Db 201 ProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGlnAsnMet 220  
 QY 1207 TTCTGTGCGGCTACGACACCAAGAGGAGGATGCTGCCAGGGGACAGCGGGGGCCCG 1266  
 Db 221 PheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGlyGlyPro 240  
 QY 1267 CACGTCCCGCTTCAAGGACACCTACTTCGTGACAGCATCGTCAGCTGGGAGAGAGC 1326  
 Db 241 HisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGlyGly 260  
 QY 1327 TGTGCGCGTAAAGGGAGTACGGGATCTACACCAAGTTCACCGCTTCTCCTCAAGTGGATC 1386  
 Db 261 CysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrAlaPheLeuLysTrpIle 280  
 QY 1387 GACAGTCCATGAACACAGGGGCTGCCCAAGGCCAAGAGCCATGCCCGGAGGTCTATA 1446  
 Db 281 AspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGluValIle 300  
 QY 1447 AGTCTCTCCATTAAAG 1464  
 Db 301 ThrSerSerProLeuLys 306

# RESULT 15

US-08-474-042-1  
 ; Sequence 1, Application US/08474042  
 ; Patent No. 5589572  
 ; GENERAL INFORMATION:  
 ; APPLICANT: King, Robert  
 ; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF INHIBITED  
 ; TITLE OF INVENTION: FORMS OF ACTIVATED BLOOD FACTORS  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Morrison & Foerster  
 ; STREET: 2000 Pennsylvania Avenue, NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20006-1888  
 ; COMPUTER READABLE FORM:  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,042  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/484,558  
 ; FILING DATE: 07-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Murashige, Kate H.  
 ; REGISTRATION NUMBER: 29,959  
 ; REFERENCE/DOCKET NUMBER: 2803-0007.02  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)887-1500  
 ; TELEFAX: (202)822-0168  
 ; TELEX: 90-4030 MRSNFOERSWSH

Alignment Scores:  
 Pred. No. 6,69e-121 Length: 306  
 Score: 1631.00 Matches: 305  
 Percent Similarity: 99.67% Conservative: 0  
 Best Local Similarity: 99.67% Mismatches: 1  
 Query Match: 60.12% Indels: 0  
 DB: 1 Gaps: 0

US-09-632-722-1 (1-1467) x US-08-330-978-1 (1-306)

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 Db 1 SerValAlaGlnAlaThrSerSerSerGlyGluAlaProAspSerIleThrTrpLysPro 20  
 QY 607 TATGATCGACCGACCTGGACCCACCGAGAACCCCTTCGACCTGTGACTTCAACCCAG 666  
 Db 21 TyrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuAspPheAsnGln 40  
 QY 667 AGCGAGCCTGAGAGGGCGACACACCTCACAGGATCGTGGAGCCAGGATCAAG 726  
 Db 41 ThrGlnProGluArgGlyAspAsnLeuThrArgIleValGlyGlnGluCysLys 60  
 QY 727 GACGGGAGTGTCCCTGGCAGCCCTCTCATCAATCAGAAACAGGGTTTCTGTGTT 786  
 Db 61 AspGlyGlyCysProThrGlnAlaLeuLeuIleAsnGlnGluAsnGlyPheCysGly 80  
 QY 787 GGAATATTCTGACGAGTCTTACATCTTAACGCGAGCCCTGTCTCTACCAAGCCAAG 846  
 Db 81 GlyThrIleLeuSerGluPheTyrIleLeuThrAlaAlaHisCysLeuTyrGlnAlaLys 100  
 QY 847 AGATTCAAGTGTAGGGTAGGGACCGGAACACCGAGAGGAGCGGCGGTGAGCGGTG 906  
 Db 101 ArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlyGluAlaVal 120  
 QY 907 CACGAGTGTGGTGTTCATCAGCACCAACCGGTTCACAAGGAGAGCTATGACTTCGAC 966  
 Db 121 HisGluValGluValIleLysHisAsnArgPheThrLysGluThrTyrAspPheAsp 140



:	TPP:	amino acid			
:	:	STANDNESS:			
:	:	TCPOLOGY:	linear		
:	:	MOLECULE TYPE:	protein		
US-08-469					
486-53					
<hr/>					
Alignment Scores:					
Pred. No.	6.83e-138	Length:	487		
Score:	1847.00	Matches:	336		
Percent Similarity:	82.81%	Conservative:	59		
Best Local Similarity:	70.44%	Mismatches:	76		
Query Match:	68.08%	Indels:	6		
DB:	1	Gaps:	3		
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Qy	13	CTGCACTCGTCTGCTCAGTGCCCTCCTGGCTGGCTCCTGTGCTGGGAAAGTCGTG	72		
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Qy	73	TTCATCCGCAGGACAGGCCAACAAACATCTCGCGAGGTGCACGAGGCCAATTCCTTT	132		
Dd	25	PheLeuProArgAspGlnAlaHisArgValLeuGlnArgAlaargAlaasnSerPhe	44		
Qy	133	CATTGAAGAGATGAAGAAAGACACTCGAAGAGAGTGCATGAAGAGACCTGCTCATAC	192		
Dd	45	LeuGluValLysGlnGlyAsnLeuGluArgGluCysLeuGluAlaCysSerLeu	64		
Qy	193	GAGAGGCCGGAGTCTTTGAGCAGCAGCACGACGAATCAATCTCGGAATAAATAC	252		
Dd	65	GluGluAlaArgGluValPheGluAspAlaGluInThrAspGluPheTrpSerLysTyr	84		
Qy	253	AAAGATGGGACCAGTGTGACACCACTCTTTGCCAGAACAACAGGCGAAATGTAAGACGCG	312		
Dd	85	LysaspGlyaspGlnCysGluGlyHisProCysLeuasnGlnGlyHisCysLysaspGly	104		
Qy	313	CTCGGGAAATACACCTGCACCTGTTTGAAGAGATTCGAAGGCAAAAACCTGTGAATATTC	372		
Dd	105	IleGlyAspTyrThrCysThrCysAlaGluGlyPheGluGlyLysasnCysGluPheSer	124		
Qy	373	ACACGGAAGCTCTGACGCTGGCAACGGGACTGTCCACAGTCTGCCACGAGGAACAG	432		
Dd	125	ThrArgGluileCysSerLeuaspAsnGlyGlyCysaspGlnPheCysargGluGluArg	144		
Qy	433	AACCTGTGTGTGTCTCTGCGCCCGCGGTGTACACCTGCTGACACGCAAGCGCTCG	492		
Dd	145	SerGluValArgCysSerCysAlaHisGlyTyrValLeuGlyAspSerLysSerCys	164		
Qy	493	ATTCCCACAGGCCCTACCCCTGTGGGAAACAGACCTTGGNACGCGAGGAGGTCAGTG	552		
Dd	165	ValSerThrGluArgPheProCysGlyLysPheThrGlnGlyArgSerArgArg-----	182		
Qy	553	GCCACGACCACGACGAGCGGGGCGCCCTGCACAGCATCATGGAAGCCATATGAT	612		
Dd	183	---TrpAlaIleHisThrSerGluaspAlaLeuaspAlaSerGluLeuGluHisTyrAsp	201		
Qy	613	GCAGCGCACTGGACCCACGAGAACCCCTTCGACCTGCTGACTTCAACACGACGACAG	672		
Dd	202	ProAlaaspLeuSerProThrGluSerSerLeuaspLeuGlyLeuAsnArgThrGlu	221		
Qy	673	CTTGAGGGGGCGAC-----AACAACTCACAGGATCTGGGAGGCCAGGAATCCAAG	726		
Dd	222	ProSerAlaGlyGluaspGlySerGlnValValArgIleValGlyArgaspCysAla	241		
Qy	727	GACGGGAGTGTCCCTGGCAGGCCCTGCTCATCATCAATGAGAAACAGGGGTTTTCTGTGT	786		
Dd	242	GluGlyGlyCysProTrpGlnAlaLeuLeuValasnGluGluAsnGluGlyPheCysGly	261		
Qy	787	GGAACATATCTGAGCGAGTTCTACATCTACGGCAGCCCACTGCTCTCTACCAAGCCAAG	846		
Dd	262	GlyThrIleLeuasnGluPheTyrValLeuThrAlaLaHisCysLeuHisGlnAlaLys	281		
Qy	847	AGATTCAAGTGTAGGTTAGGGGACCGGAAACACGAGGACGAGGAGGCGGTGAGCGGGTG	906		

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 5 LeuHisLeuValLeuLeuSerThrAlaLeuGlyGlyLeuLeuArgProAlaGlySerVal 24  
 73 TTCATCCGAGGAGGAGCCCAACACATCTTGGCGAGGCTCAGGAGCCCAATTCCTTT 132  
 25 PheLeuProArgAspGlnAlaHisArgValLeuGlnArgAlaArgAlaAsnSerPhe 44  
 133 CTGTAAGAGATGAACAAGGACACCTCCAAAGAGAGTGCATGAGAGACCTGCTCATAC 192  
 45 LeuGluGluValLysGlnGlyAsnLeuGluArgGluCysLeuGluGluAlaCysSerLeu 64  
 193 GAAGAGCCCGAGGTCTTTGAGCAGCAGCACAAGAGAAATGTAATTCGGAATAAATAC 252  
 65 GluGluAlaArgGluValPheGluAspAlaGluGlnThrAspGluPheTrpSerLysTyr 84  
 253 AAAGATGCGGACAGTGTGAGACCAAGTCTTCCAGAACACAGGCGCAATGTAAGACGCG 312  
 85 LysaspGlyAspGlnCysGluGlyHisProCysLeuAsnGlnGlyHisCysLysaspGly 104  
 313 CTCGGGGAATACACCTGCACCTGTTTACAAGGATTCGAAGCGCAAAATCTGTGAATTATC 372  
 105 IleGlyAspTyrThrCysThrCysAlaGluGlyPheGluGlyLysAsnCysGluPheSer 124  
 373 ACAGGAAGCTCTGAGCCTGGACACACGCGGACTGTGACCATGTTGTCACAGGAACAG 432  
 125 ThrArgGluIleCysSerLeuAspAsnGlyGlyCysAspGlnPheCysArgGluGluArg 144  
 433 AACCTGTGTGTGCTCTCGCCGCGGGTACACCTGGCTGACACGCGCAAGCCCTGC 492  
 145 SerGluValArgCysSerCysAlaHisGlyTyrValLeuGlyAspSerLysSerCys 164  
 493 ATTCACAGGCGCTACCTCTGTGGAAACAGACCCCTGGACACGAGGAGGTGTCATG 552  
 165 ValSerThrGluArgPheProCysGlyLysPheThrGlnGlyArgSerArgArg 182  
 553 GCCCAGGCGCACACGAGCGGGGCGCCCTGACAGCATCATGGAACCCATATCAT 612  
 183 --TrpAlaIleHisThrSerGluAspAlaLeuAspAlaSerGluLeuGluHisTyrAsp 201  
 613 GCACCGACCTGGACCCACCGAGAACCCCTTCGACCTGCTGTACTTCAACACGACGAG 672  
 202 ProAlaAspLeuSerProThrGluSerSerLeuAspLeuLeuGlyLeuAsnArgThrGlu 221  
 673 CCTGAGAGGGCGAC---AACAACTCACAGGATCTGGGAGGCCAGGAATGCAAG 726  
 222 ProSerAlaGlyGluAspGlySerGlnValValArgIleValGlyArgAspCysAla 241  
 727 GACGGGAGTGTCCCTGGCAGGCCCTCTCATCAATGAGGAAAACGAGGTTCTGTGGT 786  
 242 GluGlyGluCysProTrpGlnAlaLeuLeuValAsnGluGluAsnGluGlyPheCysGly 261  
 787 GGAATATTCTGAGCGATTTACATCCTAACCGCACCCACTGCTCTTACCAGCCAAAG 846  
 262 GlyThrIleLeuAsnGluPheTyrValLeuThrAlaAlaHisCysLeuHisGlnAlaLys 281  
 847 AGATTCAAGGTGAGGTAGGGACCGGAAACAGGAGCAGGAGGCGGTGAGCGCGGTG 906  
 282 ArgPheThrValArgValGlyAspArgAsnThrGluGlnGluGlyAsnGluMetAla 301  
 907 CACGAGGTGAGGTGTCATCAGCACACCGGTTTCAAAAGGAGACCTATGACTTCGAC 966  
 302 HisGluValGluMetThrValLysHisSerArgPheValLysGluThrTyrAspPheAsp 321  
 967 ATCCCGGTGTCGGGCTCAAGACCCCATCACCTTCGCGATGACGTCGGCGCTGCTGC 1026  
 322 IleAlaValLeuArgLeuLysThrProIleArgPheArgAsnValAlaProAlaCys 341  
 027 CTCGCCGAGCGTGACTGGGCCGAGTCCACGCTGATGACGACGAAGACGGGATTTGACG 1086

402 PheCysAlaGlyTyrAspThrGlnProGluAspAlaCysGlnGlyAspSerGlyGlyPro 421  
1267 CACGTACCCCTTCAGGACACCTACTCTGTCAGCAGCATCTGTCAGTGGGAGAGC 1326  
422 HisValThrArgPheLysAspThrPheValThrGlyIleValSerTrpGlyGly 441  
1327 TGTGCCCCCTAAGGGAGTACGGGATCTACACCAAGGTTCACCGCTTCTCCTCAAGTGGATC 1386  
442 CysAlaArgLysGlyLysPheGlyValThrLysValSerAsnPheLeuLysTrpIle 461  
1387 GACAGGTCCATGAACACAGG---GGTGTGCCCAAGGCCAAGACCAT-----GCCCGC 1437  
462 AspLysIleMetLysAlaArgAlaGlyAlaAlaGlySerArgGlyHisSerGluAlaPro 481  
1438 GAGGTCCATAACGTCTCTCCA 1458  
482 AlaThrTrpThrValProPro 488

RESULT 11  
US-08-469-658-2  
Sequence 2, Application US/08469658  
Patent No. 5917018  
GENERAL INFORMATION:  
APPLICANT: Th egeresen, Hans Christian  
APPLICANT: Holtet, Thor Las  
APPLICANT: Etzerodt, Michael  
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version  
SOFTWARE: #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,658  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/192,060  
FILING DATE: February 4, 1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 06363/002002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617 542 5070  
TELEFAX: 617 542 8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-658-2

Alignment Scores:  
Pred. No.: 3,31e-138  
Score: 1851.00  
Percent Similarity: 81.72%  
Best Local Similarity: 69.82%  
Query Match: 68.23%  
Indels: 8

45 LeuGluGluValLysGlnGlyAsnLeuGluArgGluCysLeuGluAlaCysSerLeu 64  
193 GAAGAGCCCGCGAGGTCTTTGAGGACAGCAGCAAGCAATGAATTCGGAATAAATAC 252  
65 GluGluAlaArgLysValPheGluAspAlaGluGlnThrAspGluPheTrpSerLysTrp 84  
253 AAAGATGGGACACAGTGTGAGACCACTCTTCCGACAGACAGGCGCAATGTAAACACGGC 312  
85 LysAspGlyAspGlnCysGluGlyHisProCysLeuAsnGlnGlyHisCysLysAspGly 104  
313 CTCCGGGAATACACCTGCACCTGTTTAGAGGATTCGAAGCAAAACACTGTCAATATTTC 372  
105 IleGlyAspTrpThrCysThrCysAlaGluGlyPheGluGlyLysAsnCysGluPheSer 124  
373 ACAGGAAGCTCTGCACCTGTGGAACACAGACCTGTGACCACTTCTGCCACGAGGAACAG 432  
125 ThrArgGluIleCysSerLeuAspAsnGlyGlyCysAspGlnPheCysArgGluAlaArg 144  
433 AACTCTGTGTGTCTCTGCGCGCGCGGTACACCTGTGCTGACAAACGCGCAAGCCTGC 492  
145 SerGluValArgCysSerCysAlaHisGlyTyrValLeuGlyAspAspSerLysSerCys 164  
493 ATTCCACAGGGCCCTACCTGTGGAACACAGACCTGTGGAACAGGAGGTGAGTCAAGT 552  
165 ValSerThrGluArgPheProCysGlyLysPheThrGlnGlyArgSerArgArg----- 182  
553 GCCCAGGCCACACAGCAGCGGGGAGGCCCTGACAGCATCATCATGGAAGCCATATGAT 612  
183 ---TrpAlaIleHisThrSerGluAspAlaLeuAspAlaSerGluLeuGluHisLysTrp 201  
613 GCAGCCACCTGACCCACCGAGAACCCCTGACCTGCTTCACTTCAACAGACGACGAG 672  
202 ProAlaAspLeuSerProThrGluSerSerLeuAspLeuLeuGlyLeuAsnArgThrGlu 221  
673 CCTGAGAGGGCGAC-----AACAACTCCACAGGATCGTGGGAGCCAGGAATCAAG 726  
222 ProSerAlaGlyGluAspGlySerGlnValValArgIleValGlyGlyArgAspCysAla 241  
727 GACGGGAGTGTCCCTGGGAGCCCTCTCATCAATGAGAAACAGGGTTCCTGTGTGT 786  
242 GluGlyGlyCysProThrGlnAlaLeuLeuValAsnGluAsnGluGlyPheCysGly 261  
787 GGAATATCTGACGAGTCTTACATCTTAACGCGACCCCATCTCTCTTACCAAGCCAG 846  
262 GlyThrIleLeuAsnGluPheTyrValLeuThrAlaAlaHisCysLeuHisGlnAlaLys 281  
847 AGATTCAGGTGAGGTGAGGGACCGGAACACGAGGAGGAGGCGGTGAGGCGGTG 906  
282 ArgPheThrValArgValGlyAspArgAsnThrGluGlnGluGlyAsnGluMetAla 301  
907 CACGAGTGGAGGTGTCATCAAGCACAACCGGTTCACAAGGAGACCTATGACTTCGAC 966  
302 HisGluValGluMetThrValLysHisSerArgPheValLysGluThrTrpAspPheAsp 321  
967 ATCCCGCTGTCTCCGGCTCAAGACCCCATCATCCCTTCGCGATGAACGTGGCGCTGCTGC 1026  
322 IleAlaValLeuArgLeuLysThrProIleArgPheArgAsnValAlaProAlaCys 341  
027 CTCCCGGAGGTGACTGGCGGAGTCCACGCTGATGACGAGAGAGGAGGCGGATGTGAGC 1086  
342 LeuProGluLysAspTrpAlaGluAlaThrLeuMetThrGlnLysThrGlyIleValSer 361  
087 GGCTTGGGGCCACCCACGAGAGGGCGCGGAGTCCACCAAGGTCTCAAGATGCTGGAGGTG 1146  
362 GlyPheGlyArgThrHisGluLysGlyArgLeuSerSerThrLeuLysMetLeuGluVal 381  
1147 CCCTACGTGGACCCACAGCTGCAAGCTGTCCAGCAGTTCATCATCACCCAGACATG 1206  
382 ProTyrValAspArgSerThrCysLysLeuSerSerPheThrIleThrProAsnMet 401  
207 TTCTGTCCGCTACGACACCAACAGCAGGAGTCCCTGCGAGGGGACACGGGGCGCG 1266



QY 081 GTGAGGGCTTCGGCGCCACCCACAGAGAGGGCCGGCAGTCCACAGGCTCAAGATGCTG 1140  
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QY 310 ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu 329  
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QY 141 GAGGTGCTTCAGTGGACCGCAACAGCTGCAAGCTGTCCAGCAGCTTCATCATCACCCAG 1200  
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QY 330 GluValProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln 349  
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QY 350 AsnMetPheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGly 369  
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QY 370 GlyProHisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerIrrgly 389  
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QY 381 TGGATCGCAGGTTCATGAACACAGGCGCTTGGCCAGGCGCAAGCCATGCCCGCGAG 1440  
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QY 430 ValIleThrSerSerProLeuLys 437  
Db |||||||

RESULT 9 037-3  
US-08-487-037-3  
Sequence 3, Application US/08487037  
Patent No. 5795863  
GENERAL INFORMATION:  
APPLICANT: Wolf, David L.  
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZLN: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,037  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0002.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 437 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: -40..397  
OTHER INFORMATION: /note= "Same features apply from  
OTHER INFORMATION: SEQ ID NO:2"  
FEATURE:  
NAME/KEY: Protein

LOCATION: 1..139  
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FEATURE:  
NAME/KEY: Peptide  
LOCATION: -40..0  
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LOCATION: group(17..22, 50..61, 55..70, 72..81, 89..100, 96  
LOCATION: -109, 111..124, 132..251, 150..155, 170..186,  
LOCATION: 299..313, 324..352)  
US-08-487-037-3

Alignment Scores:  
Pred. No.: 4.61e-169 Length: 437  
Score: 2241.50 Matches: 422  
Percent Similarity: 86.89% Conservative: 2  
Best Local Similarity: 86.48% Mismatches: 13  
Query Match: 82.62% Indels: 51  
DB: 1 Gaps: 1

US-09-632-722-1 (1-1467) x US-08-487-037-3 (1-437)

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QY 21 GlyGluSerLeuPheIleArgGluGlnAlaAsnAsnIleLeuAlaArgValThrArg 40  
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QY 121 GCCAATTCCTTCTTGAAGAGATGAAGAAAGACACCTCGAAAGAGAGTGCATGAAGAG 180  
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QY 241 TGAATAATAACAAAGATGCGCCAGCAGTGTGAGACAGGAGGAGGAGGAGGAGGAGG 300  
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QY 301 TGTAAAGACGGCTCGGGGAATACACCTGCACCTGTTTAGAAGGATTCGAGGCAAAAC 360  
Db |||||||



FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,9  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 437 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: both  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..139

REGION:	1..159	
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FEATURE:		
NAME/KEY:	Peptide	
LOCATION:	-40..0	
OTHER INFORMATION:		/note= "Pre-Pro leader sequen"
FEATURE:		
NAME/KEY:	Modified-site	
LOCATION:	-17	
OTHER INFORMATION:		/note= "Location of Intron A"
FEATURE:		

NAME/KEY	Modified-site	NAME/KEY	Modified-site
LOCATION: 37-38	LOCATION: 37-38	LOCATION: 46	LOCATION: 46
OTHER INFORMATION:	OTHER INFORMATION:	OTHER INFORMATION:	OTHER INFORMATION:
FEATURE: /note=	FEATURE: /note=	FEATURE: /note=	FEATURE: /note=
	"Location of Intron B"		"Location of Intron C"

NAME/KEY:	Modified-site
LOCATION:	503
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OTHER INFORMATION:	"An amino acid repre-
FEATURE:	by the greek letter Beta"
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LOCATION:	84
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OTHER INFORMATION:	"Location of interest B

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, OTHER INFORMATION: /note= "Location of Intron D"
, FEATURE:
, NAME/KEY: Modified-site
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, FEATURE:
, NAME/KEY: Modified-site
, LOCATION: (158~159)
, OTHER INFORMATION: /note= "Location of Intron F"
, FEATURE:
, NAME/KEY: Modified-site
, LOCATION: 198
, OTHER INFORMATION: /note= "Location of Intron G"
, FEATURE:
, NAME/KEY: Disulfide-bond
, LOCATION: group(17..22, 50..61, 55..70, 72..81, 88..91)
, LOCATION: ..109, 111..124, 132..251, 150..155, 170..175
, LOCATION: 299..313, 324..352)
US-08-487-037-2

Alignment Scores:
Pred. No. 1.08e-169 437
Score: 2249.50 424
Percent Similarity: 86.8% 0
Best Local Similarity: 86.8% 13
Query Match: 82.92% 51
DB: 1 Gaps: 1

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Db	21	GlyGluSerLeuPheIleArgGluGlnAlaAsnAsnIleLeuAlaArgValThrArg	40
QY	121	GCCAAATCTTCTTGAAGAGATGAAGAAAGACACCTCGAAAGAGAGTGCATGTGAAGAG	180
Db	41	AlaAsnSerPheLeuThrThrMetLysLysGlyHisLeuThrArgThrCysMetThrThr	60
QY	181	ACCTGCTCATAGGAAGGCCCGGAGGTCTTTGAGGACAGGACAGCAACGAAGAATTC	240
Db	61	ThrCysSerTyThrThrAlaArgThrValPheThrAspSerAspLysThrAsnThrPhe	80
QY	241	TGGAATAATACAAAGATGGGCACAGTGTGAGACCACTCTGCCACAACACAGGCCAAA	300
Db	81	TrpAsnLysTyLysAspGlyAspGlnCysGluThrSerProCysGlnAsnGlnGlyLys	100
QY	301	TGTAAGACGGCCTCGGGGAATACACTGCACCTGCACCTGTTTAGAAGGATTCGAAGCA	360
Db	101	CysLys**GlyLeuGlyGluTyThrCysThrCysLeuGluGlyPheGluGlyLysAsn	120
QY	361	TGTGAATATTACACAGGAACTCTGCAGCTTGACACGGGACTGTGACCACTTCGC	420
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QY	421	CACGAGGACAGAACTCTGTGGTGTGTCCTGCGCCGCGGGTACACCTGGCTGCACAA	480
Db	141	HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyTyThrLeuAlaAspAsn	160
QY	481	GGCAAGGCTCATTCCACAGGCGCTTACCCCTGGGAAACAGACCTCGAAGCAGG	540
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QY	601	AAGCCATATGATGACAGCGGACCTGGACCCCAACCGAGAACCCCTTCGACCTGCTT	660
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QY	661	AACCAAGCAGCAGCTGAGAGGGCGACAAACAACCTCACAGGATCGTGGAGGCCAGAA	720
Db	183	-----ArgIleValGlyGlnGlu	189
QY	721	TGCAGAGCGGGAGTGTCCCTGGCAGGCGCTGCTCATCATGATGAGGAAAACGAGGGTTC	780
Db	190	CysLysaspGlyGluCysProTrpGlnAlaLeuLeuIleAsnGluGluAsnGluGlyPhe	209
QY	781	TGTGGTGGAACTATTCTGAGCGAGTTCTACATCTTAACGGCAGGCCACTGTCTACCAA	840
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QY	841	GCCNAGAGATTCAGGTGAGGTGAGGGACCGGAACACGGAGCAGGAGGCGGGTGAG	900
Db	230	AlaLysArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGluGlyGlu	249
QY	901	CGGTGACAGGTGGAGGTGGTTCATCAACACACCGGTTCACNAGGAGACCTATGAC	960
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QY	961	TTCCACATCCCGTGTCCGGCTCAAGACCCCATCACCTTCGCGCATGAACGTGGCGCT	1020
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QY	1021	GCCTGCTCCCCGAGCGTGACTGGCGGAGTCCACCGTGTATGACGACAGACGGGANT	1080
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## SEQUENCE CHARACTERISTICS:

LENGTH: 448 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOPHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 1..139  
 OTHER INFORMATION: /note= "Factor X Light Chain"  
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 NAME/KEY: Region  
 LOCATION: 140..142  
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 Tripeptide"  
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 NAME/KEY: Region  
 LOCATION: 143..448  
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 PCT-US92-10242-3

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 Percent Similarity: 99.78% Conservative: 1  
 Best Local Similarity: 99.55% Mismatches: 1  
 Query Match: 89.90% Indels: 0  
 DB: 5 Gaps: 0

US-09-632-722-1 (1-1467) x PCT-US92-10242-3 (1-448)

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 21 ThrCysSerTyrGluGluAlaArgGluValPheGluAspSerAspLysThrAsnGluPhe 40  
 241 TGGAAATTAATACAAAGATGCGACAGTGTGAGACACAGTCTTGGCAGAACACGAGCAAA 300  
 41 TrpAsnLysTyrLysAspGlyAspGlnCysGluThrSerProCysGlnAsnGlnLys 60  
 301 TGTAAAGACGCGCTCGGGGAATACACCTGCACCTGTTTGAAGGATTGGAAGCAAAAC 360  
 61 CysLys\*\*\*GlyLeuGlyGluTyrThrCysThrCysLeuGluGlyPheGluGlyLysAsn 80  
 361 TGTGAATTAATACACAGGAAGCTCTGCGAGCTGGACAACGGGAGCTGTGACAGTCTGTC 420  
 81 CysGluLeuPheThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCys 100  
 421 CACGAGAACAGAACTCTGTGTTGCTCTCTGCGCCCGGGTACACCTGGCTGACAAC 480  
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 121 GlyLysAlaCysIleProThrGlyProTyrProCysGlyLysGlnThrLeuGluArg 140  
 541 AAGAGGTCACTGGCCCCAGGCCACAGCAGCAGCGGGAGGCCCTGCACAGCATCATGG 600  
 141 LysArgSerValAlaGlnAlaThrSerSerSerGlyGluAlaProAspSerIleThrTrp 160  
 601 AAGCATATGATGACGGCGACCTGGACCCACCGAGAACCCCTTCGACCTGCTGACTTC 660  
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## RESULT 8

US-08-487-037-2  
 ; Sequence 2, Application US/08487037  
 ; Patent No. 5795863  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wolf, David L.  
 ; TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 2000 pennsylvania Avenue, NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20006-1812  
 ; COMPUTER READABLE FORM: disk  
 ; MEDIUM TYPE: Floppy  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/487,037

FEATURE:  
 NAME/KEY: Region  
 LOCATION: 143..448  
 OTHER INFORMATION: /note= "Factor X Heavy Chain"  
 US-08-955-471-3

Alignment Scores:  
 Pred. No. 1.18e-184 Length: 448  
 Score: 2439.00 Matches: 446  
 Percent Similarity: 99.78% Conservative: 1  
 Best Local Similarity: 99.55% Mismatches: 1  
 Query Match: 89.90% Indels: 0  
 DB: 2 Gaps: 0

US-09-632-722-1 (1-1467) x US-08-955-471-3 (1-448)

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QY 241 TGAATAAATACAAAGATGCGACACAGTGTGACAGCAGTCTTGCAGAACAGGGCAAA 300
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DB 61 CysLys**GlyLeuGlyGluTyrThrCysThrCysLeuGluGlyPheGluGlyLysAsn 80
QY 361 TGTGAATTATTACAGGAAGCTCTGCAGCTGGACACGGGACTGTGACCACTTCTGC 420
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QY 1021 GCCTGCTCCCGAGCGTACTGGCCGAGTCCACGCTGATGACGACAGACAGCGGGATT 1080
DB 301 AlaCysLeuProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyIle 320
QY 1081 GTGAGCGGCTTCGGCGGCGCACCCACAGAGAGGCGCGGAGTCCACAGGCTCAAGATGCTG 1140
DB 321 ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu 340
QY 1141 GAGGTGCCTTACGTGGACCGCAACAGCTGCAAGCTGTCACGAGCTTCATCATCACCAG 1200
DB 341 GluValProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln 360
QY 1201 AACATGTTCTGTGCGGTACGACACCAAGCAGGAGGATGCTGCCAGGGGACAGCGGG 1260
DB 361 AsnMetPheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGly 380
QY 1261 GSCCGCAGCTCACCGCTTCAAGGACACACTTCTGTCGACAGGATGCTGAGGATGCTGAGG 1320
DB 381 GlyProHisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGly 400
QY 1321 CAGAGCTGTGCGGTAAAGGGAAGTACGGGATCTACACCAAGGTCACCGCTTCTCTCAAG 1380
DB 401 GluGlyCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrAlaPheLeuLys 420
QY 1381 TGGATCGACAGGTCCATGAAACAGAGGGCTTGGCCAAAGGCCAAGAGCCATGCCCCGGAG 1440
DB 421 TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu 440
QY 1441 GTCATAACGCTCTCTCCATTAAAG 1464
DB 441 VallieThrSerSerProLeuLys 448

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## RESULT 7

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PCT-US92-10242-3
; Sequence 3, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR0472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:

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1 AlaAsnSerPheLeuGluGluMetLysLysGlyHisLeuGluArgGluCysMetGluGlu 20  
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21 ThrCysSerTyrGluGluAlaArgGluValPheGluAspSerAspLysThrAsnGluPhe 40  
241 TGAATAAATACAAAGATCGGACCATCTGTGAGACAGTCTTGGCAGAACACAGGCGCAA 300  
41 TrpAsnLysTyrLysAspGlyAspGlnCysGluThrSerProCysGlnAsnGlnGlyLys 60  
301 TGTAAAGACGGCTCGGGGAATACACCTGCACCTGTTTAAAGATTCGAAGCGCAAAAC 360  
61 CysLys\*\*GlyLeuGlyGluTyrThrCysThrCysLeuGluGlyPheGluGlyLysAsn 80  
361 TGTGAATATTACAGGAAGCTCTCGACCTCGGACAAAGGGGACTGTACACAGTCTCGC 420  
81 CysGluLeuPheThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCys 100  
421 CACGAGGAACAGAACTGTGTGTCTCTCTGCGCCCGGGGTACACCTCGCTGCACAAAC 480  
101 HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyTyrThrLeuAlaAspAsn 120  
481 GGCAAGCCTGCATTCACAGGGCCCTACCTGTGGGAACAGACACCTGGAACCGAGG 540  
121 GlyLysAlaCysIleProThrGlyProTyrProCysGlyLysGlnThrLeuGluArgArg 140  
541 AAGAGTCACTGGCCAGGCCACACAGCAGCGGGAGGCCCTGCACAGCATCATGG 600  
141 LysArgSerValAlaGlnAlaThrSerSerSerGlyGluAlaProAspSerIleThrTrp 160  
601 AAGCATATGATGACGCGGACCTGGAGCCCGGAGAGAACCCCTTCGACCTGTGACTTC 660  
161 LysProTyrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuLeuAspPhe 180  
661 AACGACAGCGCTGAGAGGGGGACAAACACTCACAGGATCGTGGGAGCCAGGAA 720  
181 AsnGlnThrGlnProGluArgGlyAspAsnAsnLeuThrArgIleValGlyGlnGlu 200  
721 TGCAGACGGGGAGTGTCTCTGCGAGCCCTGCTCATCAATGAGAAACAGAGGTTC 780  
201 CysLysAspGlyGluCysProThrGlnAlaLeuLeuIleAsnGluAsnGluGlyPhe 220  
781 TGTGTGGAATTAFTTGAGCGATTCTACATCCTAACGCGACCCACTGTCTCTACCAA 840  
221 CysGlyGlyThrIleLeuSerGluPheTyrIleLeuThrAlaAlaHisCysLeuTyrGln 240  
841 GCCAAGAGATCAAGGTGAGGTAGGGACCGGACGAGCAGCAGGAGGCGGTGAG 900  
241 AlaLysArgPheLysValArgValGlyAspAsnThrGluGlnGluGlyGlyGlu 260  
901 GCGGTGACGAGGTGGAGGTGCTCATCAAGCAACACCGGTTCAAAAGAGACCTATGAC 960  
261 AlaValHisGluValGluValValIleLysHisAsnArgPheThrLysGluThrTyrAsp 280  
961 TTCACATCGCGGTCTCGGCTCAAGACCCCATCATCCTTCGCGATGAACGTGGCGCCT 1020  
281 PheAspIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaPro 300  
021 CCCTGCCTCCCGGAGCTGAGTGGCGGAGTCCACGCTGATGAGCGAAGAGAGGGGATT 1080  
301 AlaCysLeuProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyLe 320  
081 GTGAGCGCTTCGGGCGCACCCACGAGAGGCGCGGATCCACAGGCTCAAGATCGTG 1140  
321 ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu 340  
141 GAGGTGCTTACGTGGACCGCAACAGCTGCAAGCTGTCCAGCAGCTTCATCATCACCCAG 1200  
341 GluValProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln 360  
201 AACATGTTCTGCGGGCTACGACCAACGAGGAGGATGCTCCAGGGGAGCAGCGGG 1260  
361 AsnMetPheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGly 380

1261 GGCCGCGACGTCAACCGCTTCAAGGACACACCTTCTGTGACAGGATCGTCAAGCTGGGGA 1320  
381 GlyProHisValThrArgPheLysAspThrThrPheValThrGlyIleValSerTrpGly 400  
1321 GAGAGCTGTGCGCGTAAAGGGAAGTACGGGATCTACACCAAGGTACCGGCTTCTCAAG 1380  
401 GluGlyCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrAlaPheLys 420  
1381 TGGATCGACAGTCCATCAAAACAGGCGCTTGCCAAAGGCAAGAGCATGCCCGCGAG 1440  
421 TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu 440  
1441 CTCATAACGTCTCTCCATTAAAG 1464  
441 VallIleThrSerSerProLeuLys 448

RESULT 6  
US-08-955-471-3  
; Sequence 3, Application US/08955471  
; Patent No. 5968751  
; GENERAL INFORMATION:  
; APPLICANT: Griffin, John H.  
; APPLICANT: Masters, Rolf M.  
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
; TITLE OF INVENTION: for Inhibiting Coagulation  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Office of Patent Counsel, The Scripps  
; ADDRESSEE: Research Institute  
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/955,471  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/295,411  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSRI263.0C1  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 448 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..139  
; OTHER INFORMATION: /note= "Factor X Light Chain"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 140..142  
; OTHER INFORMATION: /note= "Factor X Connecting  
; OTHER INFORMATION: Tripeptide"

QY	421	CACGAGGAACAGAACTCTGTGGTGTGCTCTCGCCGCCGGGTACACCCCTGGCTGACAAC	480
DB	101	HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyTyrThrLeuAlaAspAsn	120
QY	481	GGCAAGGGCTCATTCCCCACAGGGCCCTACCCCTGTGGGAACACAGACCCCTGGAAACGCAGG	540
DB	121	GlyLysAlaCysIleProThrGlyProTyrProCysGlyLysGlnThrLeuGluArgArg	140
QY	541	AAGAGGTGAGTGGCCACAGGCCACAGCAGCAGCGGGAGGCCCTGACAGCATCACATGG	600
DB	141	LysArgSerValAlaGlnAlaThrSerSerSerGlyGluAlaProAspSerIleThrTyr	160
QY	601	AAGCCATATGATGCAGCGGACCTGGACCCCAACCCAGAACCCCTTCGACCTGCTTGACTTC	660
DB	161	LysProTyrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuLeuAspPhe	180
QY	661	AACCAGACGCAGCCTGAGAGGGCGCAACAACCTCACAGGATCGGCGGAGCCACAGAA	720
DB	181	AsnGlnThrGlnProGluArgGlyAspAsnAsnLeuThrArgIleValGlyGlyGlnGlu	200
QY	721	TGCAGAGACGGGAGTGTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAAACGAGGGTTTC	780
DB	201	CysLysAspGlyGluCysProTyrGlnAlaLeuLeuIleAsnGluGluAsnGluGlyPhe	220
QY	781	TGTCGTGGAACTATTCTGAGCGAGTCTTACATCTTAACGCGACGCCCACTGCTCTACCAA	840
DB	221	CysGlyGlyThrIleLeuSerGluPheTyrIleLeuThrAlaAlaHisCysLeuTyrGln	240
QY	841	GCCAAGAGATTCAAGGTGAGGGTAGGGACCGGAACACGAGCAGGAGGAGCGGTGAG	900
DB	241	AlaLysArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlyGlu	260
QY	901	GCGGTCACAGGNGGAGGTGGTCATCAACGCACACACCGGTTCAAAAGGAGACCTATGAC	960
DB	261	AlaValHisGluValGluValIleLysHisAsnArgPheThrLysGluThrTyrAsp	280
QY	961	TTGCACATCCCGCTGTCTCCGGCTCAAGACCCCACTACCTTCCGCATGAACGTCGGCCCT	1020
DB	281	PheAspIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaPro	300
QY	1021	GCCTGCCCTCCCGAGCGTGACTGGCGGAGTCACGCTGATGACGACAGACGGGGATT	1080
DB	301	AlaCysLeuProGluArgAspTyrAlaGluSerThrLeuMetThrGlnLysThrGlyIle	320
QY	1081	GTGAGCGGCTTCGGGGCCACCCACAGAGAGGGCGGCAGTCCACACAGGCTCAAGATGCTG	1140
DB	321	ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu	340
QY	1141	GAGGTGCCCTACGTGGACGCCAACAGCTGCAAGCTGTCCAGCACTTCATCATCCCCAG	1200
DB	341	GluValProTyrValAspArgAsnSerCysLysLeuSerSerSerPheIleIleThrGln	360
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US-08-295-411-3
; Sequence 3, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Westers, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1-139
; OTHER INFORMATION: /note= "Factor X Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 140..142
; OTHER INFORMATION: /note= "Factor X Connecting
; OTHER INFORMATION: Tripeptide"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 143..448
; OTHER INFORMATION: /note= "Factor X Heavy Chain"
; US-08-295-411-3

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US-09-632-722-1 (1-1467) x US-08-295-411-3 (1-448)

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US-09-632722-1 (1-1467) x US-09-367-791A-27 (1-488)

US-08-487-037-I  
: sequence 1, Application US/08487037





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Run on: August 11, 2003, 10:37:55 ; Search time 29.5 seconds  
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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

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4	2441	90.0	448	5	PCT-US92-10068-1
5	2439	89.9	448	1	US-08-295-411-3
6	2439	89.9	448	2	US-08-955-471-3
7	2439	89.9	448	5	PCT-US92-10242-3
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13	1847	68.1	487	2	US-08-469-658-53	Sequence 53, Appl
14	1631	60.1	306	1	US-08-330-978-1	Sequence 1, Appl
15	1631	60.1	306	1	US-08-474-042-1	Sequence 1, Appl
16	1631	60.1	306	1	US-08-484-558-1	Sequence 1, Appl
17	1631	60.1	306	1	US-08-774-592-1	Sequence 1, Appl
18	1354	49.9	254	1	US-08-330-978-3	Sequence 3, Appl
19	1354	49.9	254	1	US-08-474-042-3	Sequence 3, Appl
20	1354	49.9	254	1	US-08-484-558-3	Sequence 3, Appl
21	1354	49.9	254	1	US-08-774-592-3	Sequence 3, Appl
22	1305.5	48.1	247	3	US-08-944-483-49	Sequence 49, Appl
23	1289	47.5	241	1	US-08-330-978-4	Sequence 4, Appl
24	1289	47.5	241	1	US-08-474-042-4	Sequence 4, Appl
25	1289	47.5	241	1	US-08-484-558-4	Sequence 4, Appl
26	1289	47.5	241	1	US-08-774-592-4	Sequence 4, Appl
27	1051.5	38.8	461	6	5521070-2	Patent No. 5521070
28	1041.5	38.4	461	3	US-08-742-877-2	Sequence 2, Appl
29	1039.5	38.3	461	4	US-09-053-871A-21	Sequence 21, Appl
30	1002.5	37.0	415	1	US-08-073-531B-1	Sequence 1, Appl
31	1002.5	37.0	415	2	US-08-766-288-1	Sequence 1, Appl
32	996.5	36.7	415	4	US-09-118-748-2	Sequence 2, Appl
33	992.5	36.6	415	1	US-08-295-411-2	Sequence 2, Appl
34	992.5	36.6	415	1	US-08-955-471-2	Sequence 2, Appl
35	992.5	36.6	415	5	PCT-US92-10242-2	Sequence 2, Appl
36	952	35.1	444	1	US-08-475-845-2	Sequence 2, Appl
37	952	35.1	444	2	US-08-327-690-2	Sequence 2, Appl
38	952	35.1	444	2	US-08-660-289-2	Sequence 2, Appl
39	952	35.1	444	2	US-08-537-807-2	Sequence 2, Appl
40	952	35.1	444	2	US-08-871-003-2	Sequence 2, Appl
41	952	35.1	444	3	US-08-464-233-2	Sequence 2, Appl
42	952	35.1	444	3	US-09-189-607-2	Sequence 2, Appl
43	952	35.1	444	3	US-09-378-907-2	Sequence 2, Appl
44	952	35.1	444	5	PCT-US94-05779-2	Sequence 2, Appl
45	948	34.9	466	1	US-07-882-202A-4	Sequence 4, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-367-777-44  
; Sequence 44, Application US/09367777  
; Patent No. 6562598

#### GENERAL INFORMATION:

APPLICANT: Himmelspach, Michele  
Pfleiderer, Michael  
Falkner, Falko-Guenther  
Eibi, Johann  
Dorner, Friedrich  
Schlokot, Uwe  
TITLE OF INVENTION: Factor X Deletion Mutants  
and Analogues Thereof  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834

#### COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

#### CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/367,777  
FILING DATE: 10-NO. 6562598-1999  
CLASSIFICATION: <Unknown>

#### PRIOR APPLICATION DATA:

APPLICATION NUMBER: AT A 336/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCT/AT98/00046  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:



CC a recombinant protein in a plant. The method comprising expressing a  
 CC fusion protein including the recombinant protein and a cellulose  
 CC binding peptide fused to it, where the fusion protein is  
 CC compartmentalised and sequestered within plant cells, plant derived  
 CC tissue or cultured plant cells. The method is useful for obtaining large  
 CC quantities of the recombinant proteins and protein products in a simple  
 CC and cost-effective manner. Recombinant proteins may be used commercially,  
 CC such as in the food processing industry, e.g. glucamylases and glucose  
 CC isomerase are used for converting starch to high fructose corn syrup,  
 CC proteases for the hydrolysis of high molecular weight proteins and in  
 CC manufacturing leather or alcoholic beverages, pectinesterases for  
 CC pectin hydrolysis in food industry, lipases for cleaving ester linkage  
 CC in triglycerides, and for effluent treatment. The recombinant proteins  
 CC may further be used to produce protein antibiotics, which can be used  
 CC in healing processes, and to produce animal feed enzymes. The present  
 CC sequence represents a fusion protein of the invention, and comprises a  
 CC fusion of a cell signal peptide, Sig (not specified), CBD-Tma, and an  
 CC endoplasmic reticulum retaining peptide.

XX Sequence 597 AA;

Alignment Scores: 2.08e-126 Length: 597  
 Pred. No. 1874.50 Matches: 349  
 Score: 98.60% Conservative: 2  
 Percent Similarity: 98.03% Mismatches: 2  
 Best Local Similarity: 69.09% Indels: 3  
 Query Match: 22 Gaps: 2  
 DB:

US-09-632-722-1 (1-1467) x AAB31374 (1-597)

QY 373 ACAGGAGCTCTGACGCTGGACACAGGGGACTGTGACAGTCTGCCACGAGGAACAG 432  
 DB 239 ThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCysHisGluGln 258  
 QY 433 AACTCTGTGTGTCTCTCGCGCGCGGTACACCGCTGCTGACACGGCAAGCGCTGC 492  
 DB 259 AsnSerValValCysSerCysAlaArgGlyTyrThrLeuAlaAspAsnGlyLysAlaCys 278  
 QY 493 ATTCCACAGGGCCCTACCTCTGGGAAACACAGCCCTGCAACGAGGAGAGTCAAGT 552  
 DB 279 IleProThrGlyProTyrProCysGlyLysGlnThrLeuGluArgGlySerVal 298  
 QY 553 GCCCAGGCGCCACGACGAGCGGGAGCGCCCTGACAGCATCATGGAAGCCATATGAT 612  
 DB 299 AlaGlnAlaThrSerSerGlyGluAlaProAspSerIleThrTrpLysProTyrAsp 318  
 QY 613 GCACCGGACCTGGACCCCGGAGAACCCCTTGCACCTGCTGACITTCACACGACGAC 672  
 DB 319 AlaAlaAspLeuAspProThrGluAsnProPheAspLeuLeuAspPheAspGlnThrGln 338  
 QY 673 CTGAGAGGGCGCACAACTCACCC --- AGGATCGTGGAGGCCAGGAATGCAAGGAC 729  
 DB 339 ProGluArgGlyAspAsnAsnIleGluGlyArgIleValGlyGlnGluCysLysAsp 358  
 QY 730 GGGGAGTGTCCCTGGCAGGCGCTCTCATCAATGAGGAAACAGAGGTTTCTGTGGTGA 789  
 DB 359 GlyGluCysProTyrGlnAlaLeuLeuIleAsnGluAsnGluGlyPheCysGlyGly 378  
 QY 790 ACTATTCTGACGAGTCTACATCTTAACGGCACCCCACTGTCTCTACCAAGCCCAAGAGA 849  
 DB 379 ThrIleLeuSerGluPheTyrIleLeuThrAlaAlaHisCysLeuTyrGlnAlaLysArg 398  
 QY 850 TTCAGGTGAGGGTAGGGACCGGAACACGAGGAGGAGGCGGTGAGCGGCTGCAC 909  
 DB 399 PheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlyGluAlaValHis 418  
 QY 910 GAGGTGGAGGTGGTCAACAGCACACCGGTTCACAAAGGAGACCTATGACTTCGACATC 969  
 DB 419 GluValGluValValIleLysHisAsnArgPheThrLysGluThrTyrAspPheAspIle 438  
 QY 970 GCCGTGCTCCGGCTCAAGACCCCATCATCCCTTCGATGAACGTGGCGCTGCGCTC 1029

DB 439 AlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaProAlaCysLeu 458  
 QY 1030 CCCGAGCGTGACTGGCGGAGTCCACGCTGATGACGAGAGAGAGCGGGATGTGAGCGGC 1089  
 DB 459 ProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyIleValSerGly 478  
 QY 1090 TTCGGGCGCACCCACGAGAGAGGGCGGCGAGTCCACAGGCTCAAGATGCTGGAGTGCC 1149  
 DB 479 PheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeuGluValPro 498  
 QY 1150 TACGTGGACCGCAACAGCTGCAAGCTGTCCAGCAGCTTCATCATCACCACCAACATGTC 1209  
 DB 499 TyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGlnAsnMetPhe 518  
 QY 1210 TGTGCCGCTACGACACCAACGAGGAGGATGCTGCCAGGGGACAGCGGGGCGCCGAC 1269  
 DB 519 CysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGlyGlyProHis 538  
 QY 1270 GTCACCCGCTTCAAGGACACCTACTTCTGTGACAGCATCGTCAGCTGGGGAGAGAGCTGT 1329  
 DB 539 ValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGlyGluGlyCys 558  
 QY 1330 GCCCGTAAGGGGAAGTACGGGATCTACACCAAGGTCAACGCTTCTCAAGTGGATCGAC 1389  
 DB 559 AlaArgLysGlyLysTyrGlyIleThrLysValThrAlaPheLeuLysTrpIleAsp 578  
 QY 1390 AGGTCCATGAAACACGAGGGGCTTGCCCAAGGCCAAG-----AGCCAT 1431  
 DB 579 ArgSerMetLysThrArgGlyLeuProLysAlaLysProThrSerHis 594

Search completed: August 11, 2003, 10:41:41  
 Job time : 124.5 secs



99 CysLys\*\*\*GlyLeuGlyGluThrCysThrCysLeuGluGlyPheGluGlyLysAsn 118  
 361 TGTGAATTATTCACACGGAAGCTCTGCAGCCCTGGACACGGGAGCTGTGACAGTTTCG 420  
 119 CysGluLeuPheThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCys 138  
 421 CACGAGGAACAACTCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
 139 HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyThrLeuAlaAspAsn 158  
 481 GCAAGGCTGATTCACACAGGGCCCTACCCCTGTGGAAACAGACACCTGGACGACAG 540  
 159 GlyLysAlaCysIleProThrGlyProThrCysGlyLysGlnThrLeuGluArgArg 178  
 541 AAGAGGTCTAGTGGCCCGCCAGCCACAGCAGCAGCGGGAGGCCCTGTGACGATCATCG 600  
 179 LysArgArg----- 181  
 601 AAGCCATATGATGCAGCCGACCTGGACCCCGAGACCCCTTCGACCTGCTTGAATTC 660  
 181 ----- 181  
 661 AACCAGACGAGCTGAGAGGGCGCAGAACACCTCACAGGATCGTGGAGGCCAGGAA 720  
 182 -----LysArgIleValGlyGlyGlnGlu 189  
 721 TGAAGAGGGGAGTGTCCCTGGAGGGCCCTGTCTATCATGAGGAAACAGAGGTTTC 780  
 190 CysLysAspGlyGluCysProThrGlnAlaLeuLeuIleAsnGluGluAsnGlyPhe 209  
 781 TGTGTGTGAATTCCTGAGCGAGTCTATCTCTTAACGCGACGCCACTGTCTCTACAA 840  
 210 CysGlyGlyThrIleLeuAspGluPheThrIleLeuThrAlaAlaHisCysLeuThrGln 229  
 841 GCCAAGAGATTCAGGTGAGGTAGGGACCGGACCGAACACGAGCAGAGGAGGGCGGTGAG 900  
 230 AlaLysArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlyGlu 249  
 901 GCGGTGCAGGAGTGTGAGTGTCTCAAGCAGCACACCGCTTCCAAAGCAGACCTATGAC 960  
 250 AlaValHisGluValGluValIleLysHisAsnArgPheThrLysGluThrArgAsp 269  
 961 TTCGACATCCCTGCTCCGGCTCAAGACCCCGCATCCTCCGATGACCTGCGGCT 1020  
 270 PheAsnIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaPro 289  
 1021 GCTGCTCCCTGAGGCTGAGTGGCGGAGTCCACCTGATGACGAGAGAGCGGGATT 1080  
 290 AlaCysLeuProGluArgAspThrAlaGluSerThrLeuMetThrGlnLysThrGlyIle 309  
 1081 GTGAGGCTTCGGGCGCACCCACGAGAGGGCGGCGAGTCCACAGGCTCAAGATGCTG 1140  
 310 ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu 329  
 1141 GAGGTGCTTACCTGGACCCCAACAGCTGCAAGCTGTCCAGAGTTCATCATCACCCAG 1200  
 330 GluValProThrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln 349  
 1201 ACATGTTCTGTCGGCTAGCACACCAAGCAGAGAGTCCCTGCGAGGGGACCGGG 1260  
 350 AsnMetPheCysAlaGlyThrArgThrLysGlnGluAspAlaCysGlnGlyAspAlaGly 369  
 1261 GGCCGCGACCTGACCCGCTTCAAGGACACCTACTTCTGTACAGGCATCGTCAGTGGGA 1320  
 370 GlyProHisValThrArgPheLysAspThrThrPheValThrGlyIleValSerTrpGly 389  
 1321 GAGAGCTGTGCTCCGTAAGGGAAGTACGGGATCTACACCAAGTCAACCGCTTCTCTCAAG 1380  
 390 GluGlyCysAlaArgLysGlyLysThrGlyIleThrLysValThrAlaPheLeuLys 409  
 1381 TGGATCAGAGGTCATGAACACCGAGGGCTTCCCAAGCCCAAGACCATGCCCCGGAG 1440  
 1441 GTCATACGCT

410 TripileAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu 429  
 1441 GTCATACGCT  
 430 ValIleThrSerProLeuLys 437  
 RESULT 14  
 AAB31373  
 ID AAB31373 standard; Protein: 509 AA.  
 AC AAB31373;  
 XX 20-APR-2001 (first entry)  
 XX Amino acid sequence of Sig/CBD cex/ER retaining peptide fusion.  
 XX Protein production; food processing; protein antibiotic; feed enzyme;  
 KW protein L; CBD cex protein; cell signal peptide.  
 XX Synthetic.  
 OS  
 PN WO200077174-A1.  
 XX 21-DEC-2000.  
 XX 07-JUN-2000; 2000WO-IL00330.  
 XX 10-JUN-1999; 99US-0329234.  
 XX (CBDT-) CBD TECHNOLOGIES LTD.  
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 PI Shani Z, Shoseyov O;  
 DR N-PSDB; AAF24735.  
 DR WPI: 2001-112219/12.  
 XX Expressing and isolating recombinant protein in a plant, useful for  
 PT producing large quantities of recombinant proteins, by expressing a  
 PT fusion protein including a cellulose binding peptide fused to a  
 XX recombinant protein  
 PS Example: Fig 3a; 87pp; English.

The specification describes a method for expressing and isolating a recombinant protein in a plant. The method comprising expressing a fusion protein including the recombinant protein and a cellulose binding peptide fused to it, where the fusion protein is compartmentalised and sequestered within plant cells, plant derived tissue or cultured plant cells. The method is useful for obtaining large quantities of the recombinant proteins and protein products in a simple and cost-effective manner. Recombinant proteins may be used commercially, such as in the food processing industry, e.g. glucosylases and glucose isomerases are used for converting starch to high fructose corn syrup, proteases for the hydrolysis of high molecular weight proteins and in manufacturing leather or alcoholic beverages, pectinesterases for pectin hydrolysis in food industry, lipases for cleaving ester linkage in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce protein antibiotics, which can be used in healing processes, and to produce animal feed enzymes. The present sequence represents a fusion protein of the invention, and comprises a fusion of a cell signal peptide, sig (not specified), CBD cex, and an endoplasmic reticulum retaining peptide.

Sequence 509 AA;

Alignment Scores:

Pred. No.:	1,33e-126	Length:	509
Score:	1877.00	Matches:	373
Percent Similarity:	76.19%	Conservative:	11
Best Local Similarity:	74.01%	Mismatches:	54
Query Match:	69.19%	Indels:	67
	22	Gaps:	7

Db 329 GluValProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln 348  
 QY 201 AACATGTTCTGTGGCGGTACGACACCAAGCAGGAGATGCTCCAGGGGACAGCGG 1260  
 Db 349 AsnMetPheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGly 368  
 QY 261 GGCCCGCAGTCACCCCTCAAGGACACCTACTTCGTGACAGCATCGTCAGTGGGA 1320  
 Db 369 GlyProHisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGly 388  
 QY 321 GAGAGCTGTGCGCCCTAAGGAGAGTACGGGATCTACACCAAGTCCCGCTCCCAAG 1380  
 Db 389 GluGlyCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrAlaPheLeuLys 408  
 QY 381 TGGATGACAGGTCCATGAACACAGGGGCTTGCCCAAGCCAGAGCCATGCCCGGAG 1440  
 Db 409 TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu 428  
 QY 441 GTCATAACGTCCTCCATTAAG 1464  
 Db 429 ValIleThrSerSerProLeuLys 436

## RESULT 13

AA88468  
 ID AA88 468 standard; protein; 437 AA.

AC AA88468;

XX 30-Arg-1996 (first entry)

DE Human two chain factor Xai single chain precursor factor X'i.

XX Humab; factor X; single chain; factor X'i; precursor; two chain;  
 KW factor Xai; hexapeptide linker; Asn88; Ala185; proteolytic domain;  
 KW no enzymatic activity; haemostasis regulation; prevention;  
 KW treatment; thrombus formation; vasculature pathology;  
 KW thrombin induced; restenosis; inflammation; procoagulant;  
 KW wound healing; bypass factor; replacement therapy; haemophilia;  
 KW imaging; diagnosis; antibody production.

XX Homd sapiens.

XX Key Location/Qualifiers

FT Peptide 1..40

FT Protein /note= "pre-pro leader sequence"

FT Peptide 41..177

FT Protein /note= "light chain"

FT Peptide 178..183

FT Protein /note= "hexapeptide linker"

FT Domain 184..437

FT Domain /note= "heavy chain"

FT Domain 57..62

FT Domain /note= "GLA domain"

FT Misc difference 90..164

FT Misc difference 101

FT Misc difference 101

FT Misc difference 271

FT Misc difference 368

FT Disulfide-bond 56..60

FT Disulfide-bond 88..99

FT Disulfide-bond 93..108

FT Disulfide-bond 110..119

FT Disulfide-bond 127..138

FT Disulfide-bond 134..147

FT Disulfide-bond 149..162

FT Disulfide-bond 170..291

FT Disulfide-bond 190..195

FT Disulfide-bond 210..226

FT Disulfide-bond 339..353

FT Disulfide-bond 364..392

XX WO9600577-A1.

XX 11-JAN-1996.

XX 28-JUN-1995; 95WO-US08368.

XX 29-JUN-1994; 94US-0268003.

XX (CORT-) COR THERAPEUTICS INC.

XX Sinha U, Wolf DL;

XX WPI; 1996-077335/08.

XX New pro-coagulant composition to treat haemophilia - comprises

XX modified blood factors selected from Factor Xa, Factor IXa, Factor

XX VIIa and activated Protein C

XX Example 3; Fig 3; 69pp; English.

XX The present protein is the human factor X derived, single chain

XX factor X'i, a precursor for the two chain factor Xai. Factor X'i

XX differs from factor X in that the factor X activation peptide has

XX been replaced with a hexapeptide linker, and the wild type residues

XX Asp88 and Ser185 have been substtd. with Asn and Ala, respectively.

XX The hexapeptide linker comprises a proteolytic cleavage site, which

XX is cleaved to activate factor X'i, thus becoming the two chain

XX factor Xai. Factor Xai unlike its activated factor X wild type

XX homologue, factor Xa, has no enzymatic activity due to the

XX proteolytic domain amino acid substitutions Asn88 and Ala185.

XX Factor Xai can be used for the regulation of haemostasis and for

XX the prevention and treatment of thrombus formation and other

XX pathological processes in the vasculature induced by thrombin, e.g.

XX restenosis and inflammation. It may be used as a procoagulant, e.g.

XX for wound healing, as a bypass factor, in replacement therapy,

XX haemophilia treatment, in imaging and other diagnostic uses and in

XX the prodn. of antibodies which can be used in diagnosis and

XX therapy.

XX SQ Sequence 437 AA;

XX Alignment Scores:

XX Pred. No.: 4.54e-151 Length: 437

XX Score: 2217.50 Matches: 421

XX Percent Similarity: 86.68% Conservative: 2

XX Best Local Similarity: 86.27% Mismatches: 14

XX Query Match: 81.74% Indels: 51

XX DB: 17 Gaps: 3

US-09-632-722-1 (1-1467) x AAR88468 (1-437)

QY 1 ATGGGGCGCCACTGCACCTGCTCTGCTCAGTGCCTCCCTGGTGGCTGCTGCTGCTGCTC 60

Db 1 MetGlyArgProLeuHisLeuValLeuLeuSerAlaSerLeuAlaGlyLeuLeuLeu 20

QY 61 GGGAAAGTCTGTTCATCCGCGAGGAGCAGGCCAACACATCTCTGGCGAGGTCACGAGG 120

Db 21 GlyGluSerLeuPheIleArgArgGluGlnAlaAsnAsnIleLeuAlaArgValThrArg 40

QY 121 GCCAATTCCTTTCTTGAAGAGATGAAGAAGGACACCTCGAAGAGAGTGCATGGAAGAG 180

Db 41 AlaAsnSerPheLeu---ThrMetLysLysGlyHisLeuThrArgThrCysMet---Thr 58

QY 181 ACCTGCTCATACAGAGAGAGCGCGGAGTCTTTGAGGACGAGCAGCAGCAATGAATTC 240

Db 59 ThrCysSerTyrThrThrAlaArgThrValPheThrAspSerAspLysThrAsnThrPhe 78

QY 241 TGGAAATAAATACAAAGATGGCGACAGTGTGAGACCACTCTTCCAGAACACGAGGCAAA 300

Db 79 TrpAsnLysTyrLysAspGlyAspGlnCysGluThrSerProCysGlnAsnGlnGlyLys 98

QY 301 TGTAAGACGCGCTCGGGGAATACACCTGCACCTGTTTAGAAGATTTCGAAGCAAAAC 360





FT	Region	/note= "Factor X heavy chain"	
FT		238..246	
FT	Region	/note= "recognition site for Mac-1 binding"	
FT		366..373	
FT	Region	/note= "recognition site for Mac-1 binding"	
FT		423..430	
FT		/note= "recognition site for Mac-1 binding"	
XX	WO9319803-AL		
XX	27-MAY-1993		
XX	20-NOV-1992	92WO-US10068	
XX	22-NOV-1991	91US-0798221	
XX	(SCHAF) SCHAFFER S C		
PA	(SCRI) SCRIPPS RES INST		
XX	Altieri DC, Edgington TS;		
XX	WPT; 1993-182243/22		
XX	Factor X-derived polypeptide(s) inhibit binding of factor X to		
PT	Mac-1 - useful for treating thrombosis, atherosclerosis,		
PT	disseminated intravascular coagulation, septic shock etc.		
PS	Disclosure; Page 101-103; 122pp; English.		
XX	The sequence shown represents the complete amino acid sequence of		
CC	human Factor X. Fragments of this sequence corresp. to the Mac-1		
CC	(macrophage-monocyte adhesive receptor) recognition sites (see		
CC	features) of 10-25 amino acid residues may be used to inhibit Factor		
CC	Xa monocyte procoagulant activity, specifically inflammation. The		
CC	same effect may be achieved with antibodies raised to such fragments.		
CC	Typical applications include treatment of patients at risk of thrombosis		
CC	or atherosclerosis before surgery, disseminated intravascular		
CC	coagulation, septic shock, inflammation caused by infection (esp. by		
CC	herpes simplex) or autoimmune diseases, delayed hypersensitivity, etc.		
CC	The fragments also inhibit leucocyte/endothelial cell interaction and		
CC	thus regulate responses such as leucocyte recruitment, adhesion and		
CC	extravasation, haematopoiesis, antigen presentation, angiogenesis,		
CC	synchronous formation and haemostasis.		
CC	See also AAR37403-20.		
CC	(Updated on 25-MAR-2003 to correct PN field.)		
XX	Sequence 448 AA;		
SQ	Alignment: Scores:		
Prod. No.:	4.14e-165	Length:	448
Score:	2413.00	Matches:	443
Percent Similarity:	98.88%	Conservative:	0
Best Local Similarity:	98.88%	Mismatches:	5
Query Match:	88.94%	Indels:	0
DB:	14	Gaps:	0
US-09-632-722-1 (1-1467) x AAR37402 (1-448)			
QY	121	GCCAATTCCTTTCTTGAAGAGATGAAGAAGGACACCTCGAAGAGAGTGCATGGAAGAG	180
DB	1	AlaAsnSerPheLeuGluGluMetLysLysGlyHisLeuGluArgGluCysMetGluGlu	20
QY	181	ACCTGCTCATACGAAGAGGCGCGAGGTCTTTGAGGACAGGACAGACGAATGATTC	240
DB	21	ThrCysSerTyrGluGluAlaArgGluValPheGluAspSerAspLysThrAsnGluPhe	40
QY	241	TGGAATAATACAAAGATGGGACCACTGTGAGACAGTCCTTGGCAGAACACAGGGCAAA	300
DB	41	TrpAsnLysTyrLysAspGlyAspGlnCysGluThrSerProCysGlnAsnGlnGlyLys	60
QY	301	TGTAAGAGCGGCTCGGGAATACACCTGCACCTGTTTGAAGAGATTGAAGGCAAAAC	360
DB	61	CysLysAspGlyLeuGlyGluTyrThrCysThrCysLeuGluGlyPheGluGlyLysAsn	80
QY	361	TGTGAATATTACACACGGAAGCTCTGCACCTGGACACAGGGGACTGTGACCACTTGC	420
DB	81	CysGluLeuPheThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCys	100
QY	421	CACGAGAAACAGAACTCTGTGTCTCTCGCCCGGGGTACACCTGCTGCTGACAAAC	480
DB	101	HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyTyrThrLeuAlaAspAsn	120
QY	481	GGCAAGGCTGTATTCACACAGGGCCTTACCCCTGTGGGAAACAGACCTGTGAACGACAG	540
DB	121	GlyLysAlaCysIleProThrGlyProTyrProCysGlyLysGlnThrLeuGluArgArg	140
QY	541	AAGAGTCTAGTGGCCCGACACAGCAGCAGCGGGAGGCCCTTGACAGCATCATCATTG	600
DB	141	LysArgSerValAlaGlnAlaThrSerSerSerGlyGluAlaProSerPheThrTrp	160
QY	601	AAGCCATATGATGCAGCGACCTGGACCCACCCAGAACCCCTTGCACCTGCTTACATTC	660
DB	161	LysProTyrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuLeuAspPhe	180
QY	661	AACACAGCAGCCTGAGAGGGCGACACACACACCTCACCAGGATCGTGGAGGCCAGAA	720
DB	181	AsnGlnThrGlnProGlyArgGlyAspAsnAsnLeuThrArgIleValGlyGlyGlnGly	200
QY	721	TGCAAGGAGCGGGAGTGTCCCTGGCAGGCGCTCTCATCAATGAGGAAACAGAGGTTC	780
DB	201	CysLysAspGlyGluCysProThrGlnAlaLeuLeuLeuAsnGluGluAsnGluGlyPhe	220
QY	781	TGTGTGGTGAATCTTCTGAGCGAGTCTACATCTTAAGCGGACCCACTGTCTTACAA	840
DB	221	CysGlyGlyThrIleLeuSerGluPheTyrIleLeuThrAlaAlaHisCysLeuTyrGln	240
QY	841	GCAAGAGATTCAAGTGTAGGTAGGGACCGGACGACGAGCAGGAGGAGGGCGGTGAG	900
DB	241	AlaLysArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlyGlu	260
QY	901	GCGGTGCAGAGTGGAGGTGTATCAAGCACACACCGTTCACAAAGAGACCTATGAC	960
DB	261	AlaValHisGluValGluValIleLysHisAsnArgPheThrLysGluThrTyrAsp	280
QY	961	TTTCGACATCGCGTCTCCGCTCAAGACCCCTACCTTCCGATCAAGCTGCGCGCT	1020
DB	281	PheAspIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaPro	300
QY	1021	GCCTCCCTCCCGAGCGTGAAGTGGCGGAGTCCAGCTGTATGAGCAGACAGCGGGATT	1080
DB	301	AlaCysLeuProGluArgAspTrpAlaGlySerThrLeuMetThrGlnLysThrGlyIle	320
QY	1081	GTGACGCGTTCGGCGCACCCACGAGAGAGGGCGGAGTCCACAGGCTCAAGATGCTG	1140
DB	321	ValSerGlyPheGlyArgThrHisGlyLysGlyArgGlnSerThrArgLeuLysMetLeu	340
QY	1141	GAGGTGCGCTACGTGGACCGCAACAGCTGCAAGTGTCCAGCTTCATCATCATCACCAG	1200
DB	341	GluValProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln	360
QY	1201	AACATGTTCTGTGCGGCTACGACACACAGCAGGAGGATGCTGCCAGGGGAGCAGGGG	1260
DB	361	AsnMetPheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGly	380
QY	1261	GGCCCGCAGCTCACCCGCTTCAAGGACACCTACTTCTGTGACAGCATCTGCTGCGGGA	1320
DB	381	GlyProHisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGly	400
QY	1321	GAGAGCTGTGCGCCCTAAGGGGAAGTACGGGATCTACACCAAGGTCACCGCTTCTCAAG	1380
DB	401	GluGlyCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrAlaPheLeuLys	420
QY	1381	TGGATGCACAGGTCCATGAAACACAGGGGCTTGCCCAAGGCCAAGACCATGCCCGGAG	1440
DB	421	TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu	440

CC X (f1a) and f1a by comparison of wild type f1a and nfx; (2) quantifying  
 CC the impact of specific inhibitors of f1a-f1a interaction by comparison  
 CC of wild type f1a and nfx, which is useful for treatment with inhibitors  
 CC like heparin and tissue factor pathway inhibitor (TFPI); and (3)  
 CC reactions where total specificity of thrombin activation to membrane  
 CC surfaces is required, as nfx has no significant interaction with f1a in  
 CC the absence of a sufficiently charged phospholipid surface. Substitution  
 CC of wild-type arginine by asparagine at position 347 of factor X  
 CC selectively attenuates the interaction between f1a and f1a without  
 CC affecting its catalytic (thrombogenic) activity (except in the presence  
 CC of sub-saturating heparin where the rate of inhibition by antithrombin  
 CC III is 15% of normal). The present sequence represents the specifically  
 CC claimed human Factor X variant having the arginine residue at position  
 CC 347 replaced with asparagine.  
 CC NB: This sequence does not appear as such in the present patent  
 CC specification but was created using the native factor X sequence as  
 CC shown in PIR Accession Number 538554.

XX Sequence 448 AA;

Alignment Scores:  
 Pred. No. 9,23e-167 Length: 448  
 Score: 2436.00 Matches: 446  
 Percent Similarity: 99.55% Conservative: 0  
 Best Local Similarity: 99.55% Mismatches: 2  
 Query Match: 89.79% Indels: 0  
 DB: 19 Gaps: 0

US 09-632-722-1 (1-1467) x AAM66092 (1-448)

QY 121 GCAATTCCTTCTTGAAGAGATGAAGAAAGACACCTCGAAAGAGATGCTATGAAGAG 180  
 Db 1 AlaAsnSerPheLeuGluGluMetLysLysGlyHisLeuGluArgGluCysMetGluGlu 20  
 QY 181 ACCTGCTATACGAAGAGCCCGAGGTCTTTAGAGACAGCAGCAAGAGCAATGAATTC 240  
 Db 21 ThrCysSerTyrrGluGluAlaArGluValPheGluAspSerAspLysThrAsnGluPhe 40  
 QY 241 TGGNATAATACAAAGATGCGACCATGAGACACCTGCTCCAGAACACGAGGCAAA 300  
 Db 41 TriAsnLysTyrrLysAspGlyAspGlnCysGlnSerProCysGlnAsnGlnGlyLys 60  
 QY 301 TGTAAGACGCTCGGGGAATACACCTGCACCTGTTTAGAAGATTCGAAGCAAAAC 360  
 Db 61 CysLysAspGlyLeuGlyGluTyrrThrCysThrCysLeuGluGlyPheGluGlyLysAsn 80  
 QY 361 TGTGAATATTCACAGGAGCTCGAGCTGACACACGGGACCTGTGACCATGCTGC 420  
 Db 81 CysGluLeuPheThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCys 100  
 QY 421 CACGAGGAACAGAACTCTGTGTGCTCTGCGCGCGGTACACCTCGGCTGACAAAC 480  
 Db 101 HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyTyrrThrLeuAlaAspAsn 120  
 QY 481 GGCAAGGCTGCAATTCACAGGCGCTACCCCTGTGGGAAACAGACCCCTGGAGCGGAGG 540  
 Db 121 GlyLysAlaCysIleProThrGlyProTyrrProCysGlyLysGlnThrLeuGluArGarg 140  
 QY 541 AAGAGGTCAGTGGCCAGGCCACAGCAGCAGCGGGGCGCCCTGACAGCATCACATGG 600  
 Db 141 LysArgSerValAlaGlnAlaThrSerSerGlyGluAlaProAspSerIleThrTrp 160  
 QY 601 AAGCATATGATGACGCGGACCTGGACCCACAGAACCCCTTCGACCTGCTTGACTTC 660  
 Db 161 LysProTyrrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuLeuAspPhe 180  
 QY 661 AACCAAGCGCAGCTGAGAGGGGCGACAAACCTCACAGGATCGTGGGAGCGCAGGAA 720  
 Db 181 AsnGlnThrGlnProGluArgGlyAspAsnAsnLeuThrArgIleValGlyGlyGlnGlu 200  
 QY 721 TGCAGGACGGGAGTGTCCCTGCGAGCCCTGCTCATCATGAGGAAACAGAGGGTTC 780  
 Db 201 CysLysAspGlyGluCysProTrpGlnAlaLeuIleAsnGluGluAsnGluGlyPhe 220

QY 781 TGTGTGGAACTATTCTGAGCGAGTTCTACATCTTAACGGCAGCCCACTGTCCTACCAA 840  
 Db 221 CysGlyGlyThrIleLeuSerGluPheTyrrIleLeuThrAlaAlaHisCysLeuTyrrGln 240  
 QY 841 GCCAAGAGATTCAAGGTGAGGTAGGGACCGGACACCGGACGAGGAGGGGGGTGAG 900  
 Db 241 AlaLysArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlyGlu 260  
 QY 901 CGGTGTCACGAGGTGGAGTGGTTCATCAAGCACACACCGTTCACAAAGAGACACCTATGAC 960  
 Db 261 AlaValHisGluValGluValIleLysHisAsnArgPheThrLysGluThrTyrrAsp 280  
 QY 961 TTCGACATCGCGCTCTCCGGCTCAAGACCCCATCACTTCCGATGAAAGTGGCGCT 1020  
 Db 281 PheAspIleAlaValIleuLeuLysThrProIleThrPheArgMetAsnValAlaPro 300  
 QY 1021 GCCTGCTCCCGGAGCGTGTGGCCGAGTCCAGCTCCAGCTGTATGACGACAGACGCGGATT 1080  
 Db 301 AlaCysLeuProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyIle 320  
 QY 1081 GTGAGCGGCTTCGGGCGCACCCACGAGAGGGCGGCGAGTCCACGAGCTCAAGATGCTG 1140  
 Db 321 ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu 340  
 QY 1141 GAGGTCCCTACGTGGACCGCCAAACAGCTGCAAGCTGTCCAGAGCTTCATCATCACCCAG 1200  
 Db 341 GluValProTyrrValAspAsnAsnSerCysLysLeuSerSerPheIleIleThrGln 360  
 QY 1201 AACATGTTCTGCGCGGTACGACACCAAGAGGAGGATGCTGCGCAGGGGACAGCGG 1260  
 Db 361 AsnMetPheCysAlaGlyTyrrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGly 380  
 QY 1261 GCGCCGACGCTCACCGCTTCAAGGACACCTACTTCGTGACAGGATCGTCAGCTGGGA 1320  
 Db 381 GlyProHisValThrArgPheLysAspThrTyrrPheValThrGlyIleValSerTrpGly 400  
 QY 1321 GAGAGCTGTGCGCGGTAAAGGGAGTACGGGATCTACACCAAGGTCCAGCTTCCTCAAG 1380  
 Db 401 GluGlyCysAlaArgLysGlyLysTyrrGlyIleTyrrThrLysValThrAlaPheLeuLys 420  
 QY 1381 TGGATCGACAGTCCATGAAACACCGGGCTTGGCCAGGCGCAAGGACCATGCCCGGAG 1440  
 Db 421 TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu 440  
 QY 1441 GTCAATACCTCTCTCCATTAAG 1464  
 Db 441 ValIleThrSerSerProLeuLys 448

RESULT 11

AAR37402  
 ID AAR37402 standard; protein; 448 AA.

XX AAR37402;

XX 25-MAR-2003 (updated)

DT 15-SEP-1993 (first entry)

XX Factor X.

DE Homo sapiens.

KW Mac-1; macrophage-monocyte adhesive receptor; procoagulant;  
 KW inflammation; thrombosis; atherosclerosis; septic shock;  
 KW disseminated vascular coagulation; delayed hypersensitivity;  
 KW haemostasis; angiogenesis; leucocyte recruitment; adhesion.

OS Homo sapiens.

XX Location/Qualifiers  
 FH Key  
 FT Region  
 FT /note= "Factor X light chain"

FT Region  
 FT /note= "140..142"

FT Region  
 FT /note= "Factor X connecting tripeptide"  
 FT 143..448

## Alignment Scores:

Pred. No.: 4,04e-167 Length: 448  
 Score: 2441.00 Matches: 447  
 Percent Similarity: 99.78% Conservative: 0  
 Best Local Similarity: 99.78% Mismatches: 1  
 Query Match: 89.97% Indels: 0  
 DB: 14 Gaps: 0

US-09-632-722-1 (1-1467) x AAR35762 (1-448)

121 GCCAATTCCTTCTTGAAGAGATCAAGAAAGGACACCTCGAAAGAGAGTGCATGGAGAG 180  
 1 AlasnsrPheLeuGluGluMetCysGlyHisLeuGluArgGluCysMetGluGlu 20  
 181 ACCTGCTCATACGAAAGGCGCGAGGTCTTTGAGCAGCAGCAGACAGCAATGAATTC 240  
 21 ThrCysSerTyrgluGluAlaAargGluValPheGluaspSeraspLysThrAsnGluPhe 40  
 241 TGGATAATAACAAGATGGGACCACTGTGAGACCACTCTTCCCAAGAACAGGCAAA 300  
 41 TrpAsnLysTyrgluGluGluValPheGluaspSeraspLysThrAsnGluGluLys 60  
 301 TGTAAGACGCGCTCGGGGAATACACCTGCACCTGTTTGAAGATTCGAAAGCAAAAC 360  
 61 CysLysaspGlyLeuGlyGluTyrrCysThrCysLeuGluGlyPheGluGlyLysAsn 80  
 361 TGTGAATATTACACGGAAGCTCTGCAGCTGCAACCGGGACTGTGACCACTGCTGC 420  
 81 CysGluLeupheThrAargLysLeuCysSerLeuAspAsnGlyaspCysaspGlnPheCys 100  
 421 CACGAGCAACAGACTCTGTGTCTCTCTGCGCGCGGGTACACCTGGCTGACAAAC 480  
 101 HisGluGluGlnAsnSerValCysSerCysAlaAargGlyTyrrLeuAlaAspAsn 120  
 481 GGCAAGCGCTTCATCCACAGGCGCTTACCTGTGGAAACAGACCTTGGACCGCAGS 540  
 121 GlyLysAlaCysIleProThrGlyProTyrrProCysGlyLysGlnThrLeuGluAarg 140  
 541 AAGAGTCACTGCGCCAGGCCACAGCAGCGGGGAGCCCTGACAGCATCATGG 600  
 141 LysArgSerValAlaGlnAlaThrSerSerSerGlyGluAlaProaspSerIleThrTrp 160  
 601 AAGCCATATGATCAGCGGACCTGGACCCACCGAGAACCCCTTCGACCTGCTGACTTC 660  
 161 LysProTyrrAspAlaAspLeuAspProThrGluAsnProPheaspLeuLeuaspPhe 180  
 661 AACCAGAGCGCTGAGAGGCGGACAAACACCTCACCAGGATCGTGGAGCCAGGAA 720  
 181 AsnGlnThrGlnProGluAargGlyaspAsnAsnLeuThrArgIleValGlyGlnGlu 200  
 721 TGCAAGGACGGGAGTCCCTGGCAGGCGCTCTCATCAATCAGGAAACAGGGTTTC 780  
 201 CysLysaspGlyGluCysProIrrpGlnAlaLeuLeuIleAsnGluGluaspGlyPhe 220  
 781 TGTGGTGAATATTGACGAGTCTTACATCCTTAACGCGCAGCCCTGCTCTACCAA 840  
 221 CysGlyGlyThrIleLeuSerGluPheTyrrIleLeuThrAlaAlaHisCysLeuTyrrGln 240  
 841 GCCAAGAGATCAAGTGAAGGTAGGGACCGGAAACACGAGCAGGAGGAGCGGCTGAG 900  
 241 AlaLysArgPheLysValArgValGlyaspAsnThrGluGlnGluGlyGlyGlu 260  
 901 GCGGTGACGAGGTGGAGTGTATCAAGCAGCAACCGGTTTCAAGAGGACCTATGAC 960  
 261 AlaValHisGluValGluValValIleLysHisAsnArgPheThrLysGluThrTyrrasp 280  
 961 TTCGACATCCCGTCTCCGGTCAAGACCCCATCATCCTTCCGATGAACCTGGCGCT 1020  
 281 PheAspIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaPro 300  
 021 GCCTGCTCCCGAGGCTGACGTGGCGGAGTCCAGCTGATGACGACAGACGGGATT 1080

Db 301 AlaCysLeuProGluArgaspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyIle 320  
 QY 1081 GTGAGCGGCTTGGGCGCACCCACAGAGAGGCCCGCAGTCCACCAGGCTCAAGATGCTG 1140  
 Db 321 ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu 340  
 QY 1141 GAGGTCCCTACGTGGACCGCAACAGCTCAAGCTCTCCAGCAGCTTCATCATCACCAG 1200  
 Db 341 GluValProTyrrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln 360  
 QY 1201 AACATGTTCTGTCCGGCTACGACACCAAGCAGGAGGATGCTGCGAGGGGACAGCGGG 1260  
 Db 361 AsnMetPheCysAlaGlyTyrrAspThrLysGlnGluAspAlaCysGlnGlyaspSerGly 380  
 QY 1261 GCGCGCAGCTCACCGCTTCAAGCAGCAGCTTCTTCTGTCGACAGGATGTCAGCTGGGGA 1320  
 Db 381 GlyProHisValThrArgPheLysaspThrTyrrPheValThrGlyIleValSerTrpGly 400  
 QY 1321 GAGAGCTGTGCCGTAAAGGGGAAGTACGGAGTCTACACCAAGGTCCACCGCTTCTCAAG 1380  
 Db 401 GluGlyCysAlaAargLysGlyLysTyrrGlyIleTyrrLysValThrAlaPheLeuLys 420  
 QY 1381 TGGATCGCAGCTCCTCAAGAACCAAGCGGCTTGGCCAAAGGCAAGAGCCATGCCCGGAG 1440  
 Db 421 TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu 440  
 QY 1441 GTCATAACGCTCCTCCATTAAAG 1464  
 Db 441 ValIleThrSerSerProLeuLys 448

## RESULT 10

AAW66092  
 ID AAW66092 standard; peptide; 448 AA.

XX AAW66092;

DT 16-NOV-1998 (first entry)

XX Human factor X variant.

XX factor X variant; factor V; fVa; diagnostic assay; heparin; thrombin;  
 blood coagulation.

XX Homo sapiens.

XX WO9839456-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98WO-US03939.

XX 07-MAR-1997; 97US-0040047.

XX (UNIW ) UNIV WASHINGTON.

XX Miletech JP;

XX WPI; 1998-495855/42.

New human blood coagulation Factor X variant - with asparagine  
 residue at position 347, has reduced affinity for activated Factor V  
 and is useful for diagnostic assays

PS Claim 1; Page -; 42pp; English.

The invention relates to a human Factor X variant (nfx) where asparagine  
 replaces arginine at position 347. Also claimed is a method for  
 substantially reducing the affinity of human factor X for activated  
 factor V (fva) without substantially reducing the catalytic impact of  
 fva binding, by replacing arginine with asparagine at position 347. The  
 new fx variant is especially useful for in vitro assays and diagnostic  
 applications. Specifically, these include (1) quantifying the importance  
 of the interaction between the serine protease domain of activated factor

QY	355	AAAACTGTGAATTATTCACAGGAGCTCTCCAGCCCTGGACACGCGGACTGTGACCA	414	DB		458	ProGluValIleThrSerSerProLeuLys	467
DB	101	LysAsnCySGluLeuPheThrArgLysLeuCyS	120					
QY	415	TTCTGCGCAGGAGAACAGAACTCTGTGGTGTCTCTCTGCGCCCGGGGTACACCTGGCT	474					
DB	121	PheCySHISgluGluGlnAsnSerValValCyS	140					
QY	475	GACACGGCAAGCCCTGCATTCACAGGGCCCTACCCCTGTGGGAAACAGACCCCTGGAA	534					
DB	141	AspAsnGlyLysAlaCySileProThrGlyProTyrProCyS	160					
QY	535	CGCAGGAAGGTCAGTGGCCCGCAGCCACGACGAGCGGGAGGCCCTCCACAGCATC	594					
DB	161	ArgArgLysArgSerValAlaGlnAlaThrSerSerGlyAlaProAspSerIle	180					
QY	595	ACATGGAAGCATATGATGACGCGACCTGGACCCCGCAGAACCCCTTCGACCTGCT	654					
DB	181	ThrTriPlyProTyrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeu	200					
QY	655	GACTTCAACAGCAGCGAGCTGAGAGGGCGGACAACTCACCAGGATCGTGGAGGC	714					
DB	201	AspPheAsnGlnThrGlnProGluArgGlyAspAsnLeuThrArgIleValGlyGly	220					
QY	715	CAGGAATGCAAGCAGCGGAGTGTCCCTGCGCAGCCCTGCTCATCAATGAGGAAACGAG	774					
DB	221	GlnGluCySlysAspGlyGluCySProTyrGlnAlaLeuLeuIleAsnGluAsnGlu	240					
QY	775	GGTTCTGTGGTGAACATATCTGAGCGAGTTCATCTTAAGCGCAGCCCACTGTCTC	834					
DB	241	GlyPheCySglyGlyThrIleLeuSerGluPheTyrIleLeuThrAlaAlaHisCySLeu	260					
QY	835	TACCAAGCCAGAGATCAAGTGGGTAGGGAGCCGGAACACGAGCAGGAGGAGGC	894					
DB	261	TyrGlnAlaLysArgPheGlu-----GlyAspArgAsnThrGluGlnGluGly	277					
QY	895	GGTGAGCGGTGCACGAGGTGGAGGTGTCATCAACACACGCGTTCAAGAGGAGCC	954					
DB	278	GlyGluAlaValHisGluValGluValIleLysHisAsnArgPheThrLysGluThr	297					
QY	955	TATGACTTCGACATCGCGGTGTCGGCTCAAGACCCCATCACCCTCCGATGACCGTG	1014					
DB	298	TyrAspPheAspIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnVal	317					
QY	1015	CGCGCTCGCTCCCGCAGCGTACTGGCGCGAGTCCACGCTGATGACGAGAGAGCG	1074					
DB	318	AlaProAlaCySLeuProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThr	337					
QY	1075	GGGATTGTGACGGCTTCGGCGCGACCCACGAGAGGGCGGAGTCCACGAGCTCAAG	1134					
DB	338	GlyIleValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLys	357					
QY	1135	ATGCTGTGAGTGCCTACGTGGACCGCCAGCAGCTGCAAGCTGCCAGCAGCTTCATC	1194					
DB	358	MetLeuGluValProTyrValAspArgAsnSerCySLeuSerSerPheIleIle	377					
QY	1195	ACCCAGAACATGTCTCTGCGCGTACGACACCAAGCAGGAGTGTCCCGCGGGGAC	1254					
DB	378	ThrGlnAsnMetPheCySAlaGlyTyrAspThrLysGlnGluAspAlaCyS	397					
QY	1255	AGCGGGCGCGCAGTCAACCGCTTCAAGACACCTACTTGTGACGAGCATCGTCAGC	1314					
DB	398	SerGlyGlyProHisValThrArgPheLysAspThrTyrPheValThrGlyIleValSer	417					
QY	1315	TGGGAGAGACTCTGCGCGTAAAGGGAAGTACGGGATCTACACCAAGTTCACCGCTTC	1374					
DB	418	TrpGlyGluGlyCySAlaArgLysGlyAsnTyrGlyIleThrLysValThrAlaPhe	437					
QY	1375	CTCAAGTGGATCGAGGTCTCATGAAACACGAGGGCTTGCACAGCGCAAGCCATGCC	1434					
DB	438	LeuLysTrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAla	457					
QY	1435	CCGAGGTCATACGCTCTCTCCATTAAAG	1464					

DB	458	ProGluValIleThrSerSerProLeuLys	467
RESULT 9			
AAR35762			
ID	AAR35762	standard; protein; 448 AA.	
XX	AAR35762;		
XX	25-MAR-2003	(updated)	
DT	24-SEP-1993	(first entry)	
XX	Factor X (X).		
XX	PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;		
KW	Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;		
KW	exosite; catalytic activity.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	Region	1..139	
FT	Region	/note= "Factor X light chain"	
FT	Region	140..142	
FT	Region	/note= "Factor X activation"	
FT	Region	143..448	
FT	Peptide	/note= "Factor X heavy chain"	
FT	Peptide	409..423	
FT	Peptide	/note= "exosite 1"	
FT	Peptide	330..350	
FT	Peptide	/note= "exosite 2"	
FT	Peptide	330..344	
FT	Peptide	/note= "pref. PC polypeptide; claim 2, page 136"	
FT	Peptide	404..418	
FT	Peptide	/note= "pref. PC polypeptide; claim 2, page 136"	
FT	Peptide	415..429	
FT	Peptide	/note= "pref. PC polypeptide; claim 2, page 136"	
FT	Peptide	285..306	
FT	Peptide	/note= "claim 7, page 138 describes an antibody that reacts with Factor X; fragments 330-344, 404..418 and 415-429 but not with fragment 285-306"	
XX	WO9309804-A1.		
XX	27-MAY-1993.		
XX	18-NOV-1992;	92WO-US10242.	
XX	18-NOV-1991;	91US-0793989.	
XX	(SCRI )	SCRIPPS RES INST.	
XX	Griffin JH, Mesters RM;		
XX	WPI; 1993-182244/22.		
XX	Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples		
XX	Disclosure; Page 128-130; 149pp; English.		
XX	The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microm.		
XX	NR: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.		
XX	(Updated on 25-MAR-2003 to correct PN field.)		
XX	Sequence	448 AA;	



XX AC AAW75217;  
 XX DT 27-Nov-1998 (first entry)  
 XX DE Human Factor X protein analogue.  
 XX Factor X; analogue; activation cleavage site; protease; bleeding; human;  
 KW Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy.  
 XX Homi sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Peptide 1..40  
 FT Protein 41..488  
 FT /label= signal  
 FT /label= Factor\_X  
 FT Misc difference 229  
 FT /label= R6  
 FT /note= "can be residues Asp, Phe, Thr, Arg, Leu or Ser"  
 FT Misc difference 230  
 FT /label= R5  
 FT /note= "can be residues Asn, Lys, Ser, Glu, Ala, Gln,  
 FT His or Arg"  
 FT Misc difference 331  
 FT /label= R4  
 FT /note= "can be residues Asp, Ile, Ser, Met, Pro, Thr,  
 FT Arg or Lys"  
 FT Misc difference 332  
 FT /label= R3  
 FT /note= "can be residues Phe, Lys, Met, Gln, Glu, Ser,  
 FT Val, Arg or Pro"  
 FT Misc difference 333  
 FT /label= R2  
 FT /note= "can be residues Pro, Gly, Lys or Arg"  
 FT Misc difference 335  
 FT /label= R1  
 FT /note= "can be residues Ile, Val, Ser, Thr or Ala"  
 XX W098 8317-AL.  
 XX 03-SEP-1998.  
 XX 27-FEB-1998; 98WO-AT00045.  
 XX 27-FEB-1997; 97AT-0000335.  
 XX (IMMUNO) IMMUNO AG.  
 XX Dornier F, Eibl J, Fisch A, Himmelspach M, Schlokat U;  
 WPI; 1998-481211/41.  
 XX New factor X analogues with processing site for protease not active  
 PT on natural protein - and related DNA, is very stable and can be  
 PT activated in vitro or in vivo without using animal protease(s),  
 PT particularly for treating disorders of blood coagulation  
 XX Claim 4; Page -: 86pp; German.  
 XX This sequence represents a human Factor X protein analogue which has a  
 CC modification that creates a processing site for a protease in the region  
 CC of the natural F10a activation cleavage site. Such analogues are used to  
 CC generate, in vivo or in vitro, F10a analogues that can be used to control  
 CC bleeding and for treating defects of factors IX, VII or VIII, e.g. in  
 CC haemophiliacs who have developed antibodies to factors VIII and/or IX.  
 CC The encoding nucleic acid can be used in gene therapy of the same  
 CC conditions. The analogues have high stability and can be activated  
 CC without use of animal enzymes such as trypsin. Only activation is  
 CC affected, their activity is the same as the natural factor. The analogues  
 CC can be isolated as a pure single-chain pro-protein (not usually possible  
 CC because of rapid processing of the native precursor) and this converted

CC to two-chain form by subsequent activation. Activated analogues have good  
 CC stability and structural integrity and are practically free of inactive  
 CC intermediates and autolytic decomposition products.  
 CC NOTE: This sequence does not appear in the specification but has been  
 CC constructed from the wild type Factor X protein represented in Figure 1  
 CC of the specification.  
 XX SQ Sequence 488 AA;

Alignment Scores:  
 Pred. No.: 2,17e-178 Length: 488  
 Score: 2598.00 Matches: 482  
 Percent Similarity: 98.77% Conservative: 0  
 Best Local Similarity: 98.77% Mismatches: 6  
 Query Match: 95.76% Indels: 0  
 DB: 19 Gaps: 0

US-09-632-722-1 (1-1467) x AAW76217 (1-488)

QY 1 ATGGGGCGCCCACTGCACCTCGTCTGCTCAGTGTGCTCCTCGTGGCTCTCTGCTGCTC 60  
 DB 1 MetGlyArgProLeuHisLeuValLeuLeuSerAlaSerLeuAlaGlyLeuLeuLeu 20  
 QY 61 GGGGAAAGTCTGTTCATCCGAGGAGCGGAGCCACACATCTCTGGCAGGCTCAGG 120  
 DB 21 GlyGluSerLeuPheIleArgGluGlnAlaAsnAsnIleLeuAlaArgValThrArg 40  
 QY 121 GCCAATCTCTTCTTGAAGAGATGAAGAAGACACCTCGAAAGAGAGTGCATGAAGAG 180  
 DB 41 AlaAsnSerPheLeuGluGluMetLysLysGlyHisLeuGluArgGluCysMetGluGlu 60  
 QY 181 ACCTGCTCATACGAGAGGCGCGAGGTCTTTGAGACAGGACAGCAGCAATGAATTC 240  
 DB 61 ThrCysSerTyrGluGluAlaArgGluValPheGluAspSerAspLysThrAsnGluPhe 80  
 QY 241 TGAATAATACAAAGATGCGACCATGTGTGAGACCATCTTGCAGAACACAGGCAAA 300  
 DB 81 TrpAsnLysTyrLysAspGlyAspGlnCysGluThrSerProCysGlnAsnGlnGlyLys 100  
 QY 301 TGTAAAGACGGCTCGGGGAATACACCTGCACCTGTTTGAAGAGATTCGAAGCAAAAC 360  
 DB 101 CysLysAspGlyLeuGlyGluTyrThrCysThrCysLeuGluGlyPheGluLysAsn 120  
 QY 361 TGTGAATATTACACGGAAGCTCTCGACGCTGGACAGGGGACTGTGACCATGCTGC 420  
 DB 121 CysGluLeuPheThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCys 140  
 QY 421 CACGAGGACAGAACTCTGTGTGTCTCTCGCGCGCGGGGTACACCTCGCTGTCACAC 480  
 DB 141 HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyTyrThrLeuAlaAspAsn 160  
 QY 481 GGCAAGGCTTCATTCACAGGGCCCTACCCCTGTGGGAAACAGACCCCTGGAGACGAGG 540  
 DB 161 GlyLysAlaCysIleProThrGlyProTyrProCysGlyLysGlnThrLeuGluArgArg 180  
 QY 541 AAGAGTCACTGGCCAGGCGCCACACGAGCGGGGAGCCCTCGACAGCATCACATGG 600  
 DB 181 LysArgSerValAlaGlnAlaThrSerSerGlyGluAlaProaspSerIleThrTrp 200  
 QY 601 AAGCCATATGATGCAGCGGACCTGGACCCCGGAGAACCCCTTCGACCTGCTTGACTTC 660  
 DB 201 LysProTyrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuLeuAspPhe 220  
 QY 661 AACCCAGAGCGCTGAGAGGGGGGAGACAAACCTCACAGGATCGTGGAGGCCAGGAA 720  
 DB 221 AsnGlnThrGlnProGluArgGly\*\*\*\*\*Arg\*\*\*\*\*ValGlyGlyGlnGlu 240  
 QY 721 TCGAAGACGGGGAGTCTCCCTCGCAGCGCTGCTCATCATAGGAAACAGAGGGTTTC 780  
 DB 241 CysLysAspGlyGluCysProTrpGlnAlaLeuLeuIleAsnGluGluAsnGluGlyPhe 260  
 QY 781 TGTGGTGAACATATTCTGAGCGAGTTCTACATCTTAACGGCAGCCCACTGCTCTACCAA 840

Figure 1 is a line graph showing the percentage of total energy expenditure (TEE) for different activities over a 24-hour period. The Y-axis is 'Percentage of TEE' (0-100) and the X-axis is 'Time of Day' (0-24). The activities and their approximate percentages are:

Time of Day	Sleeping (%)	Resting (%)	Sitting (%)	Standing (%)	Walking (%)	Running (%)
0	40	10	10	10	10	10
4	50	10	10	10	10	10
8	40	10	10	10	10	10
12	30	10	10	10	10	20
16	30	10	10	10	10	20
20	40	10	10	10	10	10
24	40	10	10	10	10	10

RESULT 7  
AAW76217  
ID AAW7



QY	121	GCCAAATTCCTTCTTGAAGAGATGAAGAAAGGACACCTCGAAAGAGAGTGCATGGAGAG	180
Db	41	AlaAsnSerPheLeuGluGluMetLysLysGlyHisLeuGluArgGluCysMetGluGlu	60
QY	181	ACCTGCTCATACGAGAGGCGCGAGGTCTTTGAGGACAGCAGCAGAGCAATGAATTC	240
Db	61	ThrCysSerTyrGluGluAlaArgGluValPheGluAspSerAspLysThrAsnGluPhe	80
QY	241	TGGAATAATAACAAGATGCGGACCACTGTGAGACCACTCTTCCAGAAACCGGCGAAA	300
Db	81	TrpAsnLysTyrLysAspGlyAspGlnCysGluThrSerProCysGlnAsnGlnGlyLys	100
QY	301	TGTAAGACGCCCTCGGGGAATACACCTGCACCTGTTTAGAAGGATTCGAGGCAAAAC	360
Db	101	CysLysAspGlyLeuGlyGluTyrThrCysThrCysLeuGluGlyPheGluGlyLysAsn	120
QY	361	TGTGAATTATTCACAGGAAGCTCTGCAGCCTGCACAAACGGGGACTGTGACCACTTCGC	420
Db	121	CysGluLeuPheThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCys	140
QY	421	CACGAGGAACAAGACTCTGTGCTGTCTGCTGCGCCCGCGGGTACACCTGCGCTGACAAC	480
Db	141	HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyTyrThrLeuAlaAspAsn	160
QY	481	GCRAAGGCTGCATTCACAGGCGCTTACCCCTGTGGGAACACAGACCTGGAAACGAGG	540
Db	161	GlyLysAlaCysIleProThrGlyProTyrProCysGlyLysGlnThrLeuGluArg	180
QY	541	AAGAGTCAGTGGCCCGCCAGCCACGACGACGAGCGGGGCGCCCTGACAGCATCACATGG	600
Db	181	LysArgSerValAlaGlnAlaThrSerSerSerGlyGluAlaProAspSerIleThrTrp	200
QY	601	AAGCATATGATGACGCGACTCTGACCCCGCCAGACACCTTCGACCTCTTCATCTC	660
Db	201	LysProTyrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuAspPhe	220
QY	661	AACACAGCGAGCTGAGAGGCGGCACAAACCTCACAGGATCGTGGGAGGCGAGGAA	720
Db	221	AsnGlnThrGlnProGluArgGlyAspAsnAsnLeuThrArgIleValGlyGlnGlu	240
QY	721	TGCAAGGAGGGAGTGTCTCTGCGAGCGCTGTCTATCAATGAGGAAACGAGGTTTC	780
Db	241	CysLysAspGlyGluCysProTyrGlnAlaLeuLeuLeuLeuLeuLeuLeuLeuLeu	260
QY	781	TGTGTGGAACATATCTGAGGAGTCTACATCTCAACGCGAGCCACTCTCTACCAA	840
Db	261	CysGlyGlyThrIleLeuSerGluPheTyrIleLeuThrAlaAlaHisCysLeuTyrGln	280
QY	841	GCCAAAGATTCAGGTAGGTAGGGACCGGACCGGAACACGAGCAGGAGGCGGCTGAG	900
Db	281	AlaLysArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlyGlu	300
QY	901	GGGTGCGAGGTGAGTGTGTATCAAGACACACCGTTTCACAAAGGAGACCTATGAC	960
Db	301	AlaValHisGluValGluValIleLysHisAsnArgPheThrLysGluThrTyrAsp	320
QY	961	TTTCGACATCGCGTCTCGGCTCAAGACCGCCCATCACCTTCGCGATCAAGCTGCGCT	1020
Db	321	PheAsnIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaPro	340
QY	1021	GCTGCTCCCGCGAGTGTGCGGCGAGTCCACGCTGATGACCGAGAGCGGGGAT	1080
Db	341	AlaCysLeuProGluArgAspTyrAlaGluSerThrLeuMetThrGlnLysThrGlyIle	360
QY	1081	GTGAGCGGCTTGGGCGCACCGACGAGGCGCGGAGTCCACCGAGCTCAAGATGCTG	1140
Db	361	ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu	380
QY	1141	GAGGTGCCCTAGTGTGACCGCAACAGCTGCAAGCTGTCCAGCAGCTTCATCATCCAG	1200
Db	381	GluValProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln	400
QY	1201	AACATTTCTGTGCGGCTACGACACCAAGCAGGAGATGCTGCCAGGGGACAGCGGG	1260
Db	401	AsnMetPheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspAlaGly	420
QY	1261	GGCCCCACGTCACCGGCTTCAAGGACACCTACTTCTGTCAGAGGATCGTCAGCTGGGA	1320
Db	421	GlyProHisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGly	440
QY	1321	GAGAGCTGTCGCGTAAGGAGTACGAGTACACCAAGGTACACCGCTTCTCTCAAG	1380
Db	441	GluGlyCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrAlaPheLeuLys	460
QY	1381	TGATCGACAGGTCCATGAAACACGAGGCTTGGCCAAAGCCCAAGAGCCATGCCCGGAG	1440
Db	461	TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu	480
QY	1441	GTCAATACGTCCTCTCCATTAAAG	1464
Db	481	ValIleThrSerSerProLeuLys	488
RESULT 6			
ID	AAW76219	standard; Protein; 488 AA.	
XX	AAW76219;		
XX	27-NOV-1998	(first entry)	
XX	Human Factor X	protein analogue.	
XX	Factor X; analogue;	activation cleavage site; protease; bleeding; human;	
XX	Factor IX; Factor VII; Factor VIII;	haemophilia; gene therapy.	
XX	Homo sapiens.		
XX	Synthetic.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..40	
FT	Protein	/label= signal	
FT	Misc-difference	41..488	
FT	Misc-difference	/label= Factor_X	
FT	Misc-difference	174	
FT	Misc-difference	/label= R6	
FT	Misc-difference	/note= "can be residues Asp, Phe, Thr, Arg, Leu or Ser"	
FT	Misc-difference	175	
FT	Misc-difference	/label= R5	
FT	Misc-difference	/note= "can be residues Asn, Lys, Ser, Glu, Gln, Ala, His or Arg"	
FT	Misc-difference	176	
FT	Misc-difference	/label= R4	
FT	Misc-difference	/note= "can be residues Thr, Asp, Asn, Ile, Ser, Met, Pro, Arg or Lys"	
FT	Misc-difference	177	
FT	Misc-difference	/label= R3	
FT	Misc-difference	/note= "can be residues Leu, Phe, Lys, Met, Gln, Glu, Ser, Val, Arg or Pro"	
FT	Misc-difference	178	
FT	Misc-difference	/label= R2	
FT	Misc-difference	/note= "can be residues Glu, Thr, Pro, Gly, Lys or Arg"	
FT	Misc-difference	235	
FT	Misc-difference	/label= R1	
FT	Misc-difference	/note= "can be residues Val, Ser, Thr, Ile or Ala"	
XX	WO9838318-A1.		
XX	03-SEP-1998.		
XX	27-FEB-1998;	98WO-AT00046.	
XX	27-FEB-1997;	97AT-0000336.	
XX	(IMMO )	IMMUNO AG.	



QY 421 CACGAGGACAGAACTCTGTGTGTCTCTCTGCGCCGCGGTACACCTGGCTGCACAC 480  
 Db 141 HisGluGluGlnAsnSerValValCysSerCysAlaArgGlyThrLeuAlaAspAsn 160  
 QY 481 GCGAAGGCTGCATTCCTCCACAGGCGCCCTACCCCTGTGGAAACAGACCTGGAAACGAGG 540  
 Db 161 GlyLysAlaCysIleProThrGlyProThrGlyProCysGlyLysGlnThrLeuGluArg 180  
 QY 541 AAGAGGTGAGTGGCCCGCCAGCCAGCAGCAGCGGGAGGCCCTGCACATCAGATGG 600  
 Db 181 LysArgSerValAlaGlnAlaThrSerSerGlyGluAlaProAspSerIleThrTrp 200  
 QY 601 AAGCCATATGATGAGCGCCGCTGAGCCACCCAGCAGACCCCTTCGACCTGCTGACTTC 660  
 Db 201 LysProThrAspAlaAlaAspLeuAspProThrGluAsnProPheAspLeuLeuAspPhe 220  
 QY 661 AACCCAGCGCAGCTGAGAGGGGGGACACACACCTCACAGGATCGTGGAGGCGAGAA 720  
 Db 221 AsnGlnThrGlnProGluArgGlyAspAsnAsnLeuThrArgIleValGlyGlyGlnGlu 240  
 QY 721 TGCAAGGACGGGAGTGTCCCTGCGAGCGCCCTGCTCATCAATGAGGAAACAGGGTTTC 780  
 Db 241 CysLysAspGlyGluCysProTrpGlnAlaLeuLeuIleAsnGluGluAsnGluGlyPhe 260  
 QY 781 TGTGGTGAATCTTCTGAGCGAGTCTACATCCTAACGGCAGCCCTGCTCTACCAA 840  
 Db 261 CysGlyGlyThrIleLeuSerGluPheThrIleLeuThrAlaAlaHisCysLeuThrGln 280  
 QY 841 GCCAAGAGATCAAGGTGAGGTGAGGGACCGGACACGAGCAGGAGGAGCGGTGAG 900  
 Db 281 AlaLysArgPheLysValArgValGlyAspAsnThrGluGlnGluGlyGlyGlu 300  
 QY 901 GCGGTGCACGAGTGGAGTGGTGCATCAACAGCAACCGGTTCCAAAGAGACCTATGAC 960  
 Db 301 AlaValHisGluValGluValValIleLysHisAsnArgPheThrLysGluThrTrpAsp 320  
 QY 961 TTCACATCCCGTCTCCCGCTCAAGACCCCTACCTTCGCGATGAACTGGCGCCT 1020  
 Db 321 PheAspIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaPro 340  
 QY 1021 GCGTCCCTCCCGAGCGTACTGGCGGAGTCCACGCTGATGACGAGAGAGCGGGATT 1080  
 Db 341 AlaCysLeuProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyIle 360  
 QY 1081 GTGAGCGCTCGGGCCACCCACGAGAGAGCGCGGAGTCCACCGCTCAAGTGCCTG 1140  
 Db 361 ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu 380  
 QY 1141 GAGTGCCTTACGTGGACCCACACAGCTGCAAGCTGTCCAGCAGCTTCATCATCCAG 1200  
 Db 381 GluValProThrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln 400  
 QY 1201 AACATGTTCTGTCCGCTACGACACCAAGCAGGAGGATGCTCCGCGAGGAGACGCGG 1260  
 Db 401 AsnMetPheCysAlaGlyThrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGly 420  
 QY 1261 GCGCCGACGCTACCCGCTCAAGACACCTACTTCGTGACAGGATCGTCAGCTGGGA 1320  
 Db 421 GlyProHisValThrArgPheLysAspThrThrPheValThrGlyIleValSerTrpGly 440  
 QY 1321 GAGAGTGTCCCGTAAGGGAGTAGTACGGATCTACACCAAGTCAACCGCTTCTCAAG 1380  
 Db 441 GluGlyCysAlaArgLysGlyLysTyrrGlyIleThrLysValThrAlaPheLeuLys 460  
 QY 1381 TGGATCGACAGTTCATGAACAGGCGCTTGCCCAAGGCCCAAGAGCCATGCCCGGAG 1440  
 Db 461 TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu 480  
 QY 1441 GTCATACGCTCTCCATTAAAG 1464  
 Db 481 ValIleThrSerSerProLeuLys 488

## RESULT 5

AAR22512  
 ID AAR22512 standard; Protein; 488 AA.

XX AAR22512;

XX 28-JUL-1992 (first entry)

XX Mutated precursor of human Factor X analogue.

XX Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;  
 inflammation; restenosis; transplantation; haemophilia; antibodies.

XX Homo sapiens.

XX WO9204378-A.

XX 19-MAR-1992.

XX 04-SEP-1991; 91WO-US06337.

XX 04-SEP-1990; 90US-0578646.

XX (CORP-) COR THERAPEUTICS IN.

XX Wolf D;

XX WPI; 1992-114303/14.

XX New analogues of Factor XA peptide - useful for treating  
 haemophilia, thrombosis, inflammation and transplant  
 complications, for in-vivo diagnosis

XX Claim 3; Fig 1; 59pp; English.

XX The full length cDNA of human factor X was obt'd. from Dr. W.R.  
 Church, University of Vermont. This human Factor X cDNA was cloned  
 into the EcoRI site of vector pBSII (Stratagene) to obtain pBSX.  
 The HindIII-XbaI fragment of pBSX comprising the entire Factor X  
 coding region was subcloned into the HindIII-XbaI site of vector  
 M13mp19 (Mpl9X). Oligonucleotide site-directed mutagenesis was  
 then performed using oligomers to convert serine 185 on the Factor  
 X heavy chain to alanine, and to convert aspartic acid 88 on the  
 Factor X heavy chain to asparagine. Modified Factor Xa was further  
 produced by acylation e.g. with the p-nitrophenyl ester of p-toluoylic  
 acid. Modified Factor X is used to treat or prevent thrombosis;  
 inflammation; restenosis or complications of transplantation. It  
 is also used in treatment of adult respiratory distress syndrome  
 and haemophilia. The modified Factor X has no proteolytic activity  
 and interferes with the ability of endogenous factor Xa to convert  
 prothrombin to thrombin. Antibodies reactive with modified Factor X  
 are passive therapeutic agents and used for diagnosis.  
 See also AAR22513.

XX Sequence 488 AA;

XX Alignment Scores:

Pred. NO.: 4,1e-180 Length: 488  
 Score: 2622.00 Matches: 485  
 Percent Similarity: 99.80% Conservative: 2  
 Best Local Similarity: 99.39% Mismatches: 1  
 Query Match: 96.65% Indels: 0  
 DB: 13 Gaps: 0

US-09-632-722-1 (1-1467) x AAR22512 (1-488)

QY 1 ATGGGGCCCCACCTGCACCTCGCTCGCTCAGTCGCTCCCTGGCTGCTCCTCTGCTC 60  
 Db 1 MetGlyArgProLeuHisLeuValLeuSerAlaSerLeuAlaGlyLeuLeuLeu 20  
 QY 61 GGGAAAGTCTGTTCATCCGCGAGGAGCAGGCCAACACATCTCTGGGAGGCTCAGG 120  
 Db 21 GlyGluSerLeuPheIleArgGluGlnAlaAsnAlaLeuAlaArgValThrArg 40

Db 221 AsnGlnThrGlnProGluArgGlyAspAsnAsnLeuThrArgIleValGlyGlnGlu 240  
 QY 721 TGAAGAGCGGGAGTGTCCCTGGCAGGCCCTGCTCATCAATGAGAAACAGAGGTTC 780  
 Db 241 CysLysAspGlyGluCysProTrpGlnAlaLeuLeuIleAsnGluGluGlyPhe 260  
 QY 781 TGTGGTGGAACTATTCTGAGCGAGTCTACATCTTAACGGCAGCCACCTGCTTACCAA 840  
 Db 261 CysGlyGlyThrIleLeuSerGluPheTyrIleLeuThrAlaAlaHisCysLeuTyrGln 280  
 QY 841 GCCAAGAGATTCAAGGTGAGGTAGGGGACCGGACCAACAGCAGCAGAGGCGCGTGA 900  
 Db 281 AlaLysArgPheLysValArgValGlyAspArgAsnThrGluGlnGluGlyGlu 300  
 QY 901 GCGGTGCAGAGGTGGAGTGTGTCATCAAGCAGCACACCGGTTCCAAAGAGACCTATGAC 960  
 Db 301 AlaValHisGluValGluValValIleLysHisAsnArgPheThrLysGluThrTyrAsp 320  
 QY 961 TTCACATCGCCGTGCTCCGGCTCAAGACCCCATCACCTTCGGCATGACGTGGCGCT 1020  
 Db 321 PheAspIleAlaValLeuArgLeuLysThrProIleThrPheArgMetAsnValAlaPro 340  
 QY 1021 GCCTGCTCCCGAGGCTGACTGGCGGAGTCCACGCTGATGACGAGAGACGGGATT 1080  
 Db 341 AlaCysLeuProGluArgAspTrpAlaGluSerThrLeuMetThrGlnLysThrGlyIle 360  
 QY 1081 GTGAGCGGCTTCGGGCGCACCCACAGAGAGAGGGCGCGCAGTCCACAGGCTCAAGATGCTG 1140  
 Db 361 ValSerGlyPheGlyArgThrHisGluLysGlyArgGlnSerThrArgLeuLysMetLeu 380  
 QY 1141 GAGTGCCCTACGTGGACCGCAACAGCTGCAAGCTGTCCAGCAGCTTCATCATCACCCAG 1200  
 Db 381 GluValProTyrValAspArgAsnSerCysLysLeuSerSerPheIleIleThrGln 400  
 QY 1201 AACATGTTCTGTCCGGCTACGACACCAAGCAGGAGGATGCCCTGCCAGGGGACACGGG 1260  
 Db 401 AsnMetPheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGly 420  
 QY 1261 GGGCCGACGTCACCGCTTCAAGGACACCTACTTGTGACAGCATCTGTCAGCTGGGA 1320  
 Db 421 GlyProHisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGly 440  
 QY 1321 GAGAGCTGTGCGCGTAAGGGAAGTACGGGATCTACACCAAGCTCACCGCTTCCTCAAG 1380  
 Db 441 GluSerCysAlaArgLysGlyLysTyrGlyIleTyrThrLysValThrAlaPheLeuLys 460  
 QY 1381 TGGATCGACAGGTCCATGAACACGAGGGGCTTGGCCAGGCCAAGAGCCATGCCCGGAG 1440  
 Db 461 TrpIleAspArgSerMetLysThrArgGlyLeuProLysAlaLysSerHisAlaProGlu 480  
 QY 1441 GTCATAAGCTCTCTCCATTAAAG 1464  
 Db 481 ValIleThrSerSerProLeuLys 488

## RESULT 4

ID AAR22511 standard; Protein; 488 AA.  
 XX AC AAR22511;  
 XX AC AAR22511;  
 XX AC AAR22511;  
 DT 28-JUL-1992 (first entry)  
 DE Human Factor Xai.  
 XX Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;  
 KW inflammation; restenosis; transplantation; haemophilia; antibodies.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN W09204378-A.  
 XX W09204378-A.  
 PD 19-MAR-1992.

XX 04-SEP-1991; 91WO-US06337.  
 XX 04-SEP-1990; 90US-0578646.  
 PR (CORT-) COR THERAPEUTICS IN.  
 XX Wolf D;  
 XX WPI; 1992-114303/14.  
 XX New analogues of Factor Xa peptide - useful for treating  
 PT haemophilia, thrombosis, inflammation and transplant  
 PT complications, for in-vivo diagnosis  
 XX Claim 3; Fig 1; 59pp; English.  
 CC The full length cDNA for factor X (see Leytus, S.P. et al., Proc.  
 CC Natl. Acad. Sci. USA (1984) 81: 3699) was subcloned in M13mpl9 and  
 CC subjected to site specific mutagenesis to replace Ser 185 and Asp 88.  
 CC In a typical case mutagenesis was first performed with an  
 CC oligonucleotide extending Arg 142 of the light chain by Arg and Lys,  
 CC then aligning with Ile 53 of the activation peptide. When expressed  
 CC in CHO cells the truncated peptide was cleaved endogenously.  
 CC Modified Factor Xa was further produced by acylation e.g. with the  
 CC p-nitrophenyl ester of p-toluoylic acid. Factor Xai is used to  
 CC treat or prevent thrombosis; inflammation; resensitis or complications  
 CC of transplantation. It is also used in treatment of adult respiratory  
 CC distress syndrome and haemophilia. The modified factor Xai has no  
 CC proteolytic activity and interferes with the ability of endogenous  
 CC factor Xa to convert prothrombin to thrombin. Antibodies reactive  
 CC with Factor Xai are passive therapeutic agents and used for diagnosis.  
 CC See also AAR22513.  
 XX SQ Sequence 488 AA;

## Alignment Scores:

Pred. No.: 1,09e-180 Length: 488  
 Score: 2630.00 Matches: 487  
 Percent Similarity: 99.80% Conservative: 0  
 Best Local Similarity: 99.80% Mismatches: 1  
 Query Match: 96.94% Indels: 0  
 DB: 13 Gaps: 0

US-09-632-722-1 (1-1467) x AAR22511 (1-488)

QY 1 ATGGGGCGCCACTGCACCTCGCTCGTCTAGTGCCTCCCTGGCTGGCTCTCTGTGTC 60  
 Db 1 MetGlyArgProLeuHisLeuValLeuLeuSerAlaSerLeuAlaGlyLeuLeuLeu 20  
 QY 61 GGGGAAAGTCTGTTCATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
 Db 21 GlyGluSerLeuPheIleArgGluGlnAlaAsnAsnIleLeuAlaArgValThrArg 40  
 QY 121 GCCAATTCCTTTCTGAAGAGATGAAGAAGGACACCTCGAAAGAGATGTCATGAAGAG 180  
 Db 41 AlaAsnSerPheLeuGluGluMetLysLysGlyHisLeuGluArgGluCysMetGluGlu 60  
 QY 181 ACCTGCTCATAGAGAGGCGCGGAGGTCTTTGAGGACAGCAGACAGACAGATTC 240  
 Db 61 ThrCysSerTyrGluGluAlaArgGluValPheGluAspSerAspLysThrAsnGluPhe 80  
 QY 241 TGGATAAATACAAAGATGGGACCATGTGAGACCATGCTGCCAGACCATGCGGCAAA 300  
 Db 81 TrpAsnLysTyrLysAspGlyAspGlnCysGluThrSerProCysGlnAsnGlnGlyLys 100  
 QY 301 TGTAAGACGGCTCGGGGAATACACCTGCACCTGTATTAGAGGATTCGAAGGCAAAAC 360  
 Db 101 CysLysAspGlyLeuGlyGluTyrThrCysThrCysLeuGluGlyPheGluGlyLysAsn 120  
 QY 361 TGTGAATATTACACAGGAGGTCTGCACGCTGGACAACGGGACTGTGACCATCTCTGC 420  
 Db 121 CysGluLeuPheThrArgLysLeuCysSerLeuAspAsnGlyAspCysAspGlnPheCys 140







## SUMMARIES

Description

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## DESCRIPTION

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AAW76216

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01770/MWY

DT 27-NOV-1998 (first ent

Human Factor X protein.

Factor X; analogue; activation cleavage site; protease; bleeding; human;  
Factor IV. Factor VII. Factor VIII: haemophilia; gene therapy.

YY

XX

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AAB31374  
 ID AAB31374 standard; Protein; 597 AA.  
 XX  
 AC AAB31374;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of Sig/CBD-Tma/ER retaining peptide fusion.  
 XX  
 KW Protein production; food processing; protein antibiotic; feed enzyme;  
 KW protein L; CBD cex protein; cell signal peptide.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2000077174-A1.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 07-JUN-2000; 2000WO-IL00330.  
 XX  
 PR 10-JUN-1999; 99US-0329234.  
 XX  
 PA (CBD-) CBD TECHNOLOGIES LTD.  
 PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX  
 PI Shani Z, Shoseyov O;  
 XX  
 DR WPI; 2001-112219/12.  
 DR N-PSDB; AAF24738.  
 XX  
 PT Expressing and isolating recombinant protein in a plant, useful for  
 PT producing large quantities of recombinant proteins, by expressing a  
 PT fusion protein including a cellulose binding peptide fused to a  
 PT recombinant protein -  
 XX  
 PS Example; Fig 4a; 87pp; English.  
 XX  
 CC The specification describes a method for expressing and isolating  
 CC a recombinant protein in a plant. The method comprising expressing a  
 CC fusion protein including the recombinant protein and a cellulose  
 CC binding peptide fused to it, where the fusion protein is  
 CC compartmentalised and sequestered within plant cells, plant derived  
 CC tissues or cultured plant cells. The method is useful for obtaining large  
 CC quantities of the recombinant proteins and protein products in a simple  
 CC and cost-effective manner. Recombinant proteins may be used commercially,  
 CC such as in the food processing industry, e.g. glucanases and glucose  
 CC isomerase for the hydrolysis of high molecular weight proteins and in  
 CC manufacturing leather or alcoholic beverages, pectinesterases for  
 CC pectin hydrolysis in food industry, lipases for cleaving ester linkage  
 CC in triglycerides, and for effluent treatment. The recombinant proteins  
 CC may further be used to produce protein antibiotics, which can be used  
 CC in killing processes, and to produce animal feed enzymes. The present  
 CC sequence represents a fusion protein of the invention, and comprises a  
 CC fusion of a cell signal peptide, Sig (not specified), CBD-Tma, and an  
 CC endoplasmic reticulum retaining peptide.  
 XX  
 SQ Sequence 597 AA;  
 Query Match 71.2%; Score 1874.5; DB 22; Length 597;  
 Best Local Similarity 98.0%; Pred. No. 1.5e-120;  
 Matches 349; Conservative 2; Mismatches 2; Indels 3; Gaps 2;  
 QY 125 TRKLSLNGDCDQFCHEEQNSVWCSCARGYTLADNGKACIPTGYPGCKOTLERRRSV 184  
 DB 239 TRKLSLNGDCDQFCHEEQNSVWCSCARGYTLADNGKACIPTGYPGCKOTLERRRSV 298  
 QY 185 AQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDNQTPERGDNLT-RIVGQCEKD 243  
 DB 299 AQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDNQTPERGDNLT-RIVGQCEKD 358  
 QY 244 GECPWQALLINEEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEGGEAVH 303

Db 359 GECPWQALLINEEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEGGEAVH 418  
 QY 304 EVEVVIKHNRETKETYDFEDIAVLRLKTPITFRMNVAPACLPEDMAESTLMTQKTGIVSG 363  
 Db 419 EVEVVIKHNRETKETYDFEDIAVLRLKTPITFRMNVAPACLPEDMAESTLMTQKTGIVSG 478  
 QY 364 FGRTHEKGRSTRKMLVPPVYDRNSCKLSLSSFIITQNMFCAGYDTKQEDACQDSGGPH 423  
 Db 479 FGRTHEKGRSTRKMLVPPVYDRNSCKLSLSSFIITQNMFCAGYDTKQEDACQDSGGPH 538  
 QY 424 VTRFKDITYFTVGTIVSWGESCARCKGKGIYITVTAFLKWKIDRSMTKTRGLPKAK--SH 477  
 Db 539 VTRFKDITYFTVGTIVSWGESCARCKGKGIYITVTAFLKWKIDRSMTKTRGLPKAKPTSH 594

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 Job time : 86 secs

is cleaved to activate factor X'i, thus becoming the two chain factor Xai. Factor Xai unlike its activated factor X wild type homologue, factor Xa, has no enzymatic activity due to the protholytic domain amino acid substitutions Asn88 and Ala185. Factor Xai can be used for the regulation of haemostasis and for the prevention and treatment of thrombus formation and other pathological processes in the vasculature induced by thrombin, e.g. restenosis and inflammation. It may be used as a procoagulant, e.g. for wound healing, as a bypass factor, in replacement therapy, in haemophilia treatment, in imaging and other diagnostic uses and in the brodn. of antibodies which can be used in diagnosis and therapy.

Sequence 437 AA;  
Query Match 84.2%; Score 2217.5; DB 17; Length 437;  
Best Local Similarity 86.3%; Pred. No. 3.2e-144;  
Matches 421; Conservative 2; Mismatches 14; Indels 51; Gaps 3;  
1 MGRPLHLVLSASLAGLLLGSLFTRRQANNILARVTRANSFLEEMKKGHLRECEMEE 60  
|||||  
1 MGRPLHLVLSASLAGLLLGSLFTRRQANNILARVTRANSFL-TWKKGHLTRTCM-T 58  
|||||  
61 TCSYEAAREVFEDSKTNEFWNKYKDGQCTSPQNOGKCKDGLGEVTCCTCLEGFEKN 120  
|||||  
59 TCSYTTARTVFTSDKTNTFWNKYKDGQCTSPQNOGKCKKGLGEVTCCTCLEGFEKN 118  
|||||  
121 CELFTFKLCSLNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180  
|||||  
119 CELFTFKLCSLNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 178  
|||||  
181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPDLDFNQTQPERGDNNTLRIVGGOE 240  
|||  
179 KRR-----KRIVGGOE 189  
241 CKDGECPWQALLINEEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDNRTEQEEGE 300  
|||||  
190 CKDGECPWQALLINEEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDNRTEQEEGE 249  
|||||  
301 AVHEVEVVKHNRFTKETDYDFDAVLRLKTPITFRMNVAPACLPEDWAESTLMTQKGI 360  
|||||  
250 AVHEVEVVKHNRFTKETDYDFDAVLRLKTPITFRMNVAPACLPEDWAESTLMTQKGI 309  
|||||  
361 VSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 420  
|||||  
310 VSGFGRTHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 369  
|||||  
421 GPHVTRFKDFTYFTGIVSGESCARKGKYGIYTKVTAFLKWDIDRSMTKTLGPKAKSHAPE 480  
|||||  
370 GPHVTRFKDFTYFTGIVSGESCARKGKYGIYTKVTAFLKWDIDRSMTKTLGPKAKSHAPE 429  
|||||  
481 VITSSPLK 488  
430 VITSSPLK 437

RESULT 14  
AAB31373  
ID AAB31373 standard; Protein; 509 AA.  
XX AAB31373;  
AC AAB31373;  
XX AAB31373;  
DT 20-APR-2001 (first entry)  
XX Amino acid sequence of Sig/CBD cex/ER retaining peptide fusion.  
XX Protein production; food processing; protein antibiotic; feed enzyme;  
KW protein L; CBD cex protein; cell signal peptide.  
XX Synthetic.  
XX WO200077174-A1.

21-DEC-2000.  
XX 07-JUN-2000; 2000WO-IL00330.  
XX 10-JUN-1999; 99US-0329234.  
XX (CBDT-) CBD TECHNOLOGIES LTD.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
XX Shani Z, Shoseyov O;  
XX WPI; 2001-112219/12.  
DR N-PSDB; AAF24735.  
XX  
PT Expressing and isolating recombinant protein in a plant, useful for  
PT producing large quantities of recombinant proteins, by expressing a  
PT fusion protein including a cellulose binding peptide fused to a  
PT recombinant protein  
XX  
PS Example; Fig 3a; 87pp; English.  
CC The specification describes a method for expressing and isolating a  
CC recombinant protein in a plant. The method comprising expressing a  
CC fusion protein including the recombinant protein and a cellulose  
CC binding peptide fused to it, where the fusion protein is  
CC compartmentalised and sequestered within plant cells, plant derived  
CC tissue or cultured plant cells. The method is useful for obtaining large  
CC quantities of the recombinant proteins and protein products in a simple  
CC and cost-effective manner. Recombinant proteins may be used commercially,  
CC such as in the food processing industry, e.g. glucanases and glucose  
CC isomerases are used for converting starch to high fructose corn syrup.  
CC proteinases for the hydrolysis of high molecular weight proteins and in  
CC manufacturing leather or alcoholic beverages, pectinesterases for  
CC pectin hydrolysis in food industry, lipases for cleaving ester linkage  
CC in triglycerides, and for effluent treatment. The recombinant proteins  
CC may further be used to produce protein antibiotics, which can be used  
CC in healing processes, and to produce animal feed enzymes. The present  
CC sequence represents a fusion protein of the invention, and comprises a  
CC fusion of a cell signal peptide, Sig (not specified), CBD cex, and an  
CC endoplasmic reticulum retaining peptide.  
XX  
SQ Sequence 509 AA;

Query Match 71.2%; Score 1874.5; DB 22; Length 509;  
Best Local Similarity 98.0%; Pred. No. 1.3e-120;  
Matches 349; Conservative 2; Mismatches 2; Indels 3; Gaps 2;  
QY 125 TRKLCSLNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERRKRSV 184  
|||||  
Db 151 TRKLCSLNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERRKRSV 210  
|||||  
QY 185 AOATSSSGEAPDSITWKPYDAADLDPTENPDLDFNQTQPERGDNNTLRIVGGOECKD 243  
|||||  
Db 211 AOATSSSGEAPDSITWKPYDAADLDPTENPDLDFNQTQPERGDNNTLRIVGGOECKD 270  
|||||  
QY 244 GECPPWQALLINEEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDNRTEQEEGEAVH 303  
|||||  
Db 271 GECPPWQALLINEEGFCGGTILSEFYILTAHCLYQAKRFKRVGRDNRTEQEEGEAVH 330  
|||||  
QY 304 EVEVVKHNRFTKETDYDFDAVLRLKTPITFRMNVAPACLPEDWAESTLMTQKGIYSG 363  
|||||  
Db 331 EVEVVKHNRFTKETDYDFDAVLRLKTPITFRMNVAPACLPEDWAESTLMTQKGIYSG 390  
|||||  
QY 364 FGRTHEKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 423  
|||||  
Db 391 FGRTHEKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 450  
|||||  
QY 424 VTRFKDFTYFTGIVSGESCARKGKYGIYTKVTAFLKWDIDRSMTKTLGPKAK--SH 477  
|||||  
Db 451 VTRFKDFTYFTGIVSGESCARKGKYGIYTKVTAFLKWDIDRSMTKTLGPKAKPTSH 506  
|||||



DR WPI; 1992-114303/14.

XX New analogues of Factor Xa peptide - useful for treating

PT haemophilia, thrombosis, inflammation and transplant

PT complications, for in-vivo diagnosis

XX

PS Claim 7; Fig 1; 59pp; English.

XX

CC The full length cDNA of human factor X (Mpl9X) was converted to

CC encode a truncated form of human Factor X, designated rx', by deletion

CC of the activation peptide by oligonucleotide site directed mutagenesis.

CC An oligonucleotide was used to align Arg 142 following the

CC C-terminus of the Factor X light chain with Ile 53 of the Factor X

CC activation peptide (1st residue of the heavy chain). When expressed

CC in CHO cells the truncated peptide was cleaved endogenously.

CC Modified Factor Xa was further produced by acylation e.g. with the

CC p-nitrophenyl ester of p-toluylic acid. Factor rx' is used to

CC treat or prevent thrombosis; inflammation; restenosis or complications

CC of transplantation. It is also used in treatment of adult respiratory

CC distress syndrome and haemophilia. The modified factor X has no

CC proteolytic activity and interferes with the ability of endogenous

CC factor Xa to convert prothrombin to thrombin. Antibodies reactive

CC with Factor rx' are passive therapeutic agents and used for diagnosis.

CC See also AAR22512.

XX

SQ Sequence 436 AA;

Query Match 88.0%; Score 2317; DB 13; Length 436;

Best Local Similarity 89.1%; Pred. No. 4.7e-151;

Matches 435; Conservative 0; Mismatches 1; Indels 52; Gaps 1;

QY 1 MGRPLHLVLLSASLAGLLLLGSLFIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60

DB 1 MGRPLHLVLLSASLAGLLLLGSLFIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60

QY 61 TCSYEAREVFESDKTNEFWNKYKDGQDCETSPCONQKCKDGLGYCTCTLEGEGKN 120

DB 61 TCSYEAREVFESDKTNEFWNKYKDGQDCETSPCONQKCKDGLGYCTCTLEGEGKN 120

QY 121 CELFTRKLCSLDNGDCDQFCHEQNSVVCSCARGYTLADNGKACIPTGPYPCGKQTLERR 180

DB 121 CELFTRKLCSLDNGDCDQFCHEQNSVVCSCARGYTLADNGKACIPTGPYPCGKQTLERR 180

QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDPNQTPERGNNLTRIVGGQE 240

DB 181 K-----RIVGGQE 188

QY 241 CKDGCPQWALLINEEGFCGGTILSEFYILTAACHLYQAKRFKRVVGRNTEQEGGE 300

DB 189 CKDGCPQWALLINEEGFCGGTILSEFYILTAACHLYQAKRFKRVVGRNTEQEGGE 248

QY 301 AVHEVEVVIKHNRTKETDYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQGTGI 360

DB 249 AVHEVEVVIKHNRTKETDYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQGTGI 308

QY 361 VSGFGTRHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYTKQEDACOGDSG 420

DB 309 VSGFGTRHKGROSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYTKQEDACOGDSG 368

QY 421 GPHVTRFKDPTFYVTGIVSGECSKARGKYGYTKVTAFLKWDIDRSMTKRLGPKAKSHAPE 480

DB 369 GPHVTRFKDPTFYVTGIVSGECSKARGKYGYTKVTAFLKWDIDRSMTKRLGPKAKSHAPE 428

QY 481 VITSSPLK 488

DB 429 VITSSPLK 436

RESULT 13

AAR88468

ID AAR88468 standard; protein; 437 AA.

XX

AC AAR88468;

XX 30-AUG-1996 (first entry)

Human two chain factor Xa1 single chain precursor factor X'i.

Human; factor X; single chain; factor X'i; precursor; two chain;

factor Xa1; hexapeptide linker; Asp88; Ala185; proteolytic domain;

no enzymatic activity; haemostasis regulation; prevention;

treatment; thrombus formation; vasculature pathology;

thrombin induced; restenosis; inflammation; procoagulant;

wound healing; bypass factor; replacement therapy; haemophilia;

imaging; diagnosis; antibody production.

XX Homo sapiens.

XX

Key Location/Qualifiers

Peptide 1..40

Protein /note= "pre-pro leader sequence"

41..177

Peptide /note= "light chain"

178..183

Protein /note= "hexapeptide linker"

184..437

Domain /note= "heavy chain"

57..62

Domain /note= "GLA domain"

90..164

Misc-difference 101 /note= "growth factor domains"

Misc-difference 271 /note= "given as beta in specification"

Misc-difference 368 /note= "wild type Asp substd. with Asn"

Disulfide-bond 56..60 /note= "wild type Ser substd. with Ala"

Disulfide-bond 88..99

Disulfide-bond 93..108

Disulfide-bond 110..119

Disulfide-bond 127..138

Disulfide-bond 134..147

Disulfide-bond 149..162

Disulfide-bond 170..291

Disulfide-bond 190..195

Disulfide-bond 210..226

Disulfide-bond 339..353

Disulfide-bond 364..392

XX WO9600577-A1.

XX 11-JAN-1996.

XX 28-JUN-1995; 95WO-US08368.

XX 29-JUN-1994; 94US-0268003.

XX (CORT-) COR THERAPEUTICS INC.

XX Sinha U, Wolf DL;

XX WPI; 1996-077335/08.

XX New pro-coagulant composition to treat haemophilia - comprises

XX modified blood factors selected from Factor Xa, Factor IXa, Factor

XX VIII and activated Protein C

XX Example 3; Fig 3; 69pp; English.

XX The present protein is the human factor X derived, single chain

XX factor X'i, a precursor for the two chain factor Xa1. Factor X'i

XX differs from factor X in that the factor X activation peptide has

XX been replaced with a hexapeptide linker, and the wild type residues

XX Asp88 and Ser185 have been substd. with Asn and Ala, respectively.

XX The hexapeptide linker comprises a proteolytic cleavage site, which

QY 401 NMFCAGYDTKQEDACQDGGPHVTRFKDTEYVTGIVSWGECARCKGYIYTKVTAFK 460  
 DB 361 NMFCAGYDTKQEDACQDGGPHVTRFKDTEYVTGIVSWGECARCKGYIYTKVTAFK 420  
 QY 461 WIDRSMKTRGLPKAKSHAPEVITSSPLK 488  
 DB 421 WIDRSMKTRGLPKAKSHAPEVITSSPLK 448

## RESULT 11

ID AAR37402 standard; protein; 448 AA.

AC AAR37402;

DT 25-MAR-2003 (updated)

DT 15-SEP-1993 (first entry)

DE Factor X.

XX Mac-1; macrophage-monocyte adhesive receptor; procoagulant;  
 KW inflammation; thrombosis; atherosclerosis; septic shock;  
 KW disseminated vascular coagulation; delayed hypersensitivity;  
 KW haemostasis; angiogenesis; leucocyte recruitment; adhesion.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..139

FT /note= "Factor X light chain"

FT Region 140..142

FT /note= "Factor X connecting tripeptide"

FT Region 143..448

FT /note= "Factor X heavy chain"

FT Region 238..246

FT /note= "recognition site for Mac-1 binding"

FT Region 366..373

FT /note= "recognition site for Mac-1 binding"

FT Region 423..430

FT /note= "recognition site for Mac-1 binding"

XX WO9309803-A1.

PN 27-MAY-1993.

PD 20-NOV-1992; 92WO-US10068.

XX 22-NOV-1991; 91US-0798221.

XX (SCHAF) SCHAFER S C.

PA (SCHAF) SCRIPPS RES INST.

XX Altieri DC, Edgington TS;

PI WPI; 1993-182243/22.

XX Factor X-derived polypeptide(s) inhibit binding of factor X to

XX Mac-1 - useful for treating thrombosis, atherosclerosis,

XX disseminated intravascular coagulation, septic shock etc.

XX Disclosure; Page 101-103; 122pp; English.

XX The sequence shown represents the complete amino acid sequence of  
 XX human Factor X. Fragments of this sequence corresp. to the Mac-1  
 XX (macrophage-monocyte adhesive receptor) recognition sites (see  
 XX features) of 10-25 amino acid residues may be used to inhibit Factor  
 XX Xa monocyte procoagulant activity, specifically inflammation. The  
 XX same effect may be achieved with antibodies raised to such fragments.  
 XX Typical applications include treatment of patients at risk of thrombosis  
 XX or atherosclerosis before surgery, disseminated intravascular  
 XX coagulation, septic shock, inflammation caused by infection (esp. by  
 XX herpes simplex) or autoimmune diseases, delayed hypersensitivity, etc.

CC The fragments also inhibit leucocyte/endothelial cell interaction and  
 CC thus regulate responses such as leucocyte recruitment, adhesion and  
 CC extravasation, haematopoiesis, antigen presentation, angiogenesis,  
 CC syncytial formation and haemostasis.

CC See also AAR37403-20.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 448 AA;

Query Match 91.6%; Score 2413; DB 14; Length 448;

Best Local Similarity 98.9%; Pred. No. 1.3e-157; Indels 0; Gaps 0;  
 Matches 443; Conservative 0; Mismatches 5;

QY 41 ANSFLEEMKKGHLRECEMEETCSYEEAREVEFEDSKTNEFWNKYKDGQCEPQNOGK 100

DB 1 ANSFLEEMKKGHLRECEMEETCSYEEAREVEFEDSKTNEFWNKYKDGQCEPQNOGK 60

QY 101 CKDGLGEYTCLEGEFEGKNCLEFTRKLCSLDNGDCDQFCHHEQNSVVCSCARGYTLADN 160

DB 61 CKDGLGEYTCLEGEFEGKNCLEFTRKLCSLDNGDCDQFCHHEQNSVVCSCARGYTLADN 120

QY 161 GKACIPTGYPGCGKOTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENFDLLDF 220

DB 121 GKACIPTGYPGCGKOTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENFDLLDF 180

QY 221 NQTOPERGDNNLTRIVGGQCKGCECPWQALLINEENEGFCGGTILSEFYILTAHCLYQ 280

DB 181 NQTOPERGDNNLTRIVGGQCKGCECPWQALLINEENEGFCGGTILSEFYILTAHCLYQ 240

QY 281 AKRFKRVGDRNTEQEGGEAVHEVVIKINRRTKETDYDFDIAVLRLKPTIFRMNVAP 340

DB 241 AKRFKRVGDRNTEQEGGEAVHEVVIKINRRTKETDYDFDIAVLRLKPTIFRMNVAP 300

QY 341 ACLPERDWAESTLMTQKTGIVSGFGRTHKEGRQSTRLKMLEVPYVDRNSCKLSSFFITQ 400

DB 301 ACLPERDWAESTLMTQKTGIVSGFGRTHKEGRQSTRLKMLEVPYVDRNSCKLSSFFITQ 360

QY 401 NMFCAGYDTKQEDACQDGGPHVTRFKDTEYVTGIVSWGECARCKGYIYTKVTAFK 460

DB 361 NMFCAGYDTKQEDACQDGGPHVTRFKDTEYVTGIVSWGECARCKGYIYTKVTAFK 420

QY 461 WIDRSMKTRGLPKAKSHAPEVITSSPLK 488

DB 421 WIDRSMKTRGLPKAKSHAPEVITSSPLK 448

## RESULT 12

ID AAR22513 standard; Protein; 436 AA.

XX AC AAR22513;

XX 28-JUL-1992 (first entry)

XX Truncated precursor of human Factor Xai.

XX Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;  
 KW inflammation; restenosis; transplantation; haemophilia; antibodies.

XX Homo sapiens.

XX WO9204378-A.

XX 19-MAR-1992.

XX 04-SEP-1991; 91WO-US06337.

XX 04-SEP-1990; 90US-0578646.

XX (CORT-) COR THERAPEUTICS IN.

XX Wolf D;

XX

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DR WPI; 1993-182244/22.
XX
PT Serine protease derived-polypeptide(s) and anti-peptide
PT antibodies - for inhibiting coagulation and assaying for the
PT presence of serine protease in fluid samples
XX
XX
PS Discl osure; Page 128-130; 149pp; English.
XX
XX The PC polypeptides indicated in the Features Table inhibit
CC coagulation (they prevent binding of serine protease to natural
CC substrates), esp. when admin. to give an intravascular blood
CC cond. of 0.1-100 (pref. 0.5-10) microm.
CC NB: sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
CC in the specification but have not yet been added to the SEQUENCE
CC LISTING.
CC (Updated on 25-WAR-2003 to correct PN field.)
XX
XX Sequence 448 AA;
SQ
Query Match 92.7%; Score 2441; DB 14; Length 448;
Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 41 ANSFLEEMKKGHLERECMEETCSYEAREVFEDSDKTNEFWNKYKDGQCETSPQNOGK 100
Db 1 ANSFLEEMKKGHLERECMEETCSYEAREVFEDSDKTNEFWNKYKDGQCETSPQNOGK 60
QY 101 CKDGLGEYTCCTLEGEGKNCLEFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADN 160
Db 61 CKDGLGEYTCCTLEGEGKNCLEFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADN 120
QY 161 GKACIPGYPGCGQTLEERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTEPNFDLLDF 220
Db 121 GKACIPGYPGCGQTLEERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTEPNFDLLDF 180
QY 221 NOTQPERGDNNTTRIVGGQCKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQ 280
Db 181 NOTQPERGDNNTTRIVGGQCKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQ 240
QY 281 AKRFKVRVGRDNTQEEGGEAVHEVVIKHNRTKTYDFDIAVLRLKPTIFRNMVAP 340
Db 241 AKRFKVRVGRDNTQEEGGEAVHEVVIKHNRTKTYDFDIAVLRLKPTIFRNMVAP 300
QY 341 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQ 400
Db 301 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQ 360
QY 401 NMFACAGYDTKQEDACQDGGPHVTRFKDITFYFTGIVSGEGSCARKGKIYTKVTAFLK 460
Db 361 NMFACAGYDTKQEDACQDGGPHVTRFKDITFYFTGIVSGEGSCARKGKIYTKVTAFLK 420
QY 461 WIDRSMKTRGLPKAKSHAPEVITSSPLK 488
Db 421 WIDRSMKTRGLPKAKSHAPEVITSSPLK 448
RESULT 10
AAW66092
ID AAW66092 standard; peptide; 448 AA.
XX
XX AAW66092;
AC AAW66092;
XX
XX 16-NOV-1998 (first entry)
DT
DE Human factor X variant.
XX
XX factor X variant; factor V; fVa; diagnostic assay; heparin; thrombin;
KW blood coagulation.
XX
XX Homo sapiens.
XX
XX WO98 9456-A1.
PN
XX

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PD 11-SEP-1998.
XX
XX 05-MAR-1998; 98WO-US03939.
XX
XX 07-MAR-1997; 97US-0040047.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Miletich JP;
XX
XX WPI; 1998-495855/42.
XX
XX New human blood coagulation Factor X variant - with asparagine
XX residue at position 347, has reduced affinity for activated Factor V
XX and is useful for diagnostic assays
XX
XX Claim 1; Page -; 42pp; English.
XX
XX The invention relates to a human Factor X variant (nfx) where asparagine
XX replaces arginine at position 347. Also claimed is a method for
XX substantially reducing the affinity of human Factor X for activated
XX Factor V (fva) without substantially reducing the catalytic impact of
XX fva binding, by replacing arginine with asparagine at position 347. The
XX new fX variant is especially useful for in vitro assays and diagnostic
XX applications. Specifically, these include (1) quantifying the importance
XX of the interaction between the serine protease domain of activated Factor
XX X (fXa) and fva by comparison of wild type fXa and nfx; (2) quantifying
XX the impact of specific inhibitors of fva-fXa interaction by comparison
XX of wild type fXa and nfx, which is useful for treatment with inhibitors
XX like heparin and tissue factor pathway inhibitor (TFPI); and (3)
XX reactions where total specificity of thrombin activation to membrane
XX surfaces is required, as nfx has no significant interaction with fva in
XX the absence of a sufficiently charged phospholipid surface. Substitution
XX of wild-type arginine by asparagine at position 347 of factor X
XX selectively attenuates the interaction between fXa and fva without
XX affecting its catalytic (thrombogenic) activity (except in the presence
XX of sub-saturating heparin where the rate of inhibition by antithrombin
XX III is 15% of normal). The present sequence represents the specifically
XX claimed human Factor X variant having the arginine residue at position
XX 347 replaced with asparagine.
XX NB: This sequence does not appear as such in the present patent
XX specification but was created using the native factor X sequence as
XX shown in PIR Accession Number 538554.
XX
XX Sequence 448 AA;
Query Match 92.5%; Score 2436; DB 19; Length 448;
Best Local Similarity 99.6%; Pred. No. 3.3e-159;
Matches 446; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 41 ANSFLEEMKKGHLERECMEETCSYEAREVFEDSDKTNEFWNKYKDGQCETSPQNOGK 100
Db 1 ANSFLEEMKKGHLERECMEETCSYEAREVFEDSDKTNEFWNKYKDGQCETSPQNOGK 60
QY 101 CKDGLGEYTCCTLEGEGKNCLEFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADN 160
Db 61 CKDGLGEYTCCTLEGEGKNCLEFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADN 120
QY 161 GKACIPGYPGCGQTLEERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTEPNFDLLDF 220
Db 121 GKACIPGYPGCGQTLEERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTEPNFDLLDF 180
QY 221 NOTQPERGDNNTTRIVGGQCKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQ 280
Db 181 NOTQPERGDNNTTRIVGGQCKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQ 240
QY 281 AKRFKVRVGRDNTQEEGGEAVHEVVIKHNRTKTYDFDIAVLRLKPTIFRNMVAP 340
Db 241 AKRFKVRVGRDNTQEEGGEAVHEVVIKHNRTKTYDFDIAVLRLKPTIFRNMVAP 300
QY 341 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQ 400
Db 301 ACLPERDWAESTLMTQKTGIVSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQ 360

```

XX detection; drug modelling; restriction protease.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX FT Domain 108..153

XX FT Domain /label= EGF2 domain

XX FT Domain 154..165

XX FT Domain /label= EGF2 domain

XX FT Domain 166..216

XX FT Domain /label= Activating domain

XX FT Domain 217..454

XX FT Domain /label= catalytic domain

XX W0977737-A1.

XX 18-DEC-1997.

XX PF 11-JUN-1997; 97WO-EP03027.

XX PR 06-JUL-1996; 96EP-0110959.

XX PR 11-JUN-1996; 96EP-0109288.

XX PR 22-JUN-1996; 96EP-0110109.

XX PA (BOE) BOEHRINGER MANNHEIM GMBH.

XX PI Hopfer K, Kopetzki E;

XX DR WPI; 1998-052304/05.

XX DR N-PSDB; AAV10462.

XX PT Non-glycosylated, truncated forms of factor IX family protein with

XX PT serine protease activity - used to screen for specific modulators

XX PT and to assay factor IXa

XX PS Disclosure; Fig 3; 49pp; German.

XX CC This sequence represents a human factor X protease. This protein is used

XX CC in the construction of a novel non-glycosylated protein and truncated

XX CC and ymogen forms of this protein, which have serine protease activity.

XX CC The protein is composed of various domains from a factor IX family

XX CC protein, namely a catalytic domain (CD) N-terminally bound to a

XX CC zymogen-activating domain (ZAD), N-terminally bound to an EGF1 and/or

XX CC EGF2 domain (EGF = epidermal growth factor-like domain). Such proteins

XX CC are used to identify activators/inhibitors of factor IX family proteins

XX CC (potentially useful as regulators of coagulation, fibrinolysis and

XX CC homeostasis). The protein in zymogen form is also useful in assays for

XX CC detecting factor IXa activity in aqueous solution (specifically in body

XX CC fluids). The protein can be used to produce co-crystals with protease

XX CC variants or inhibitors for X-ray structural analysis and drug modelling

XX CC and is restriction proteases in biotechnology. These truncated proteins

XX CC have the same specificity as factor IX family proteases and can be

XX CC produced in prokaryotes in a form that allows production of active enzyme

XX CC by conversion to native form and enzymatic cleavage.

XX SQ Sequence 467 AA;

Query Match 95.1%; Score 2505.5; DB 19; Length 467;

Best Local Similarity 98.5%; Pred. No. 6e-164;

Matches 463; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 19 LLGESLFIREEQANNILARYTRANSFLEEMKGLHRECEMEETCSYEAREVFEDSDKTN 78

DB 1 LLGESLFIREEQANNILARYTRANSFLEEMKGLHRECEMEETCSYEAREVFEDSDKTN 60

QY EFNNKYKDGQCFSTPCONQKCKGLGEVTCCTCLEGFEKNCLETRKLCISLDNGDCDQ 138

DB EFNNKYKDGQCFSTPCONQKCKGLGEVTCCTCLEGFEKNCLETRKLCISLDNGDCDQ 120

QY 61 EFNNKYKDGQCFSTPCONQKCKGLGEVTCCTCLEGFEKNCLETRKLCISLDNGDCDQ 120

DB 139 FCHEQNSVVCARGYTLADNGKACIPGYPGCGQTLERRKRSVAQATSSSGEAPDSI 198

QY 121 FCHEQNSVVCARGYTLADNGKACIPGYPGCGQTLERRKRSVAQATSSSGEAPDSI 180

DB 121 FCHEQNSVVCARGYTLADNGKACIPGYPGCGQTLERRKRSVAQATSSSGEAPDSI 180

QY 199 TWKPYDAADLDPTENPFDLLDFNQTPQERGDNNLTRYVGQCKDGECPWQALLINEENE 258

DB 181 TWKPYDAADLDPTENPFDLLDFNQTPQERGDNNLTRYVGQCKDGECPWQALLINEENE 240

QY 259 GFCGGTILSEFYILTAHCLYQAKRFVVGDRNTEQEEGGEAVHEVVIKHNRTKET 318

DB 241 GFCGGTILSEFYILTAHCLYQAKRFE--GDRNTEQEEGGEAVHEVVIKHNRTKET 297

QY 319 YDFDIAVRLKTPITFRMNVAPACLPEDRWAESTLMTQKTGIVSGFGRTHKGRQSTRLK 378

DB 298 YDFDIAVRLKTPITFRMNVAPACLPEDRWAESTLMTQKTGIVSGFGRTHKGRQSTRLK 357

QY 379 MLEVPYVDRNSCKLSSFIITQNMFCAGYDTQEDACQDSCGSGPHVTRFKDIYFVTGIYS 438

DB 358 MLEVPYVDRNSCKLSSFIITQNMFCAGYDTQEDACQDSCGSGPHVTRFKDIYFVTGIYS 417

QY 439 WGESCARKGYIYTKVTAFLKWDIRSMKTRGLPKAKSHAPEVITSSPLK 488

DB 418 WGESCARKGYIYTKVTAFLKWDIRSMKTRGLPKAKSHAPEVITSSPLK 467

RESULT 9

AAR35762

ID AAR35762 standard; protein; 448 AA.

XX AC

XX AC AAR35762;

XX DT 25-MAR-2003 (updated)

XX DT 24-SEP-1993 (first entry)

XX XX

XX DE Factor X (X).

XX DE PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;

XX KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding;

XX KW exosite; catalytic activity.

XX XX

XX OS Homo sapiens.

XX XX

XX FH Key

XX FH Region 1..139

XX FT /note= "Factor X light chain"

XX FT Region 140..142

XX FT /note= "Factor X activation"

XX FT Region 143..448

XX FT /note= "Factor X heavy chain"

XX FT Peptide 409..423

XX FT /note= "exosite 1"

XX FT Peptide 330..350

XX FT /note= "exosite 2"

XX FT Peptide 330..344

XX FT /note= "pref. PC polypeptide; claim 2, page 136"

XX FT Peptide 404..418

XX FT /note= "pref. PC polypeptide; claim 2, page 136"

XX FT Peptide 415..429

XX FT /note= "pref. PC polypeptide; claim 2, page 136"

XX FT Peptide 285..306

XX FT /note= "claim 7, page 138 describes an antibody

XX FT that reacts with Factor X; fragments

XX FT 330-344, 404..418 and 415-429 but not

XX FT with fragment 285-306"

XX XX

XX PN W09309804-A1.

XX PN 27-MAY-1993.

XX PF 18-NOV-1992; 92WO-US10242.

XX PR 18-NOV-1991; 91US-0793989.

XX XX (SCRI) SCRIPPS RES INST.

XX PI Griffin JH, Mesters RM;

421 GPHVTRFDYFTVTVGIVSGWSCARKGKGIYTKVTAFLKWLDRSMKTRGLPKAKSHAPE 480  
481 VITSSPLK 488  
481 VITSSPLK 488

RESULT 7  
AAW76217  
XX AAW7217 standard; Protein; 488 AA.  
XX AAW7217:  
XX AAW7217:  
XX 27-JUN-1998 (first entry)  
XX Human Factor X protein analogue.  
XX Factor X; analogue; activation cleavage site; protease; bleeding; human;  
XX Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy.  
XX Homo sapiens.  
XX Synthetic.

XX Key Location/Qualifiers  
XX Peptide 1..40  
XX Protein /label= signal  
XX /label= Factor\_X  
XX /label= R6  
XX /label= R5  
XX /label= R4  
XX /label= R3  
XX /label= R2  
XX /label= R1  
XX /label= R0  
XX /label= R1  
XX /label= R2  
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XX /label= R4  
XX /label= R5  
XX /label= R6  
XX /label= R7  
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XX /label= R97  
XX /label= R98  
XX /label= R99  
XX /label= R100

XX 27-FEB-1997; 97AT-0000335.  
XX (IMMO) IMMUNO AG.  
XX Dornier F, Elbl J, Fisch A, Himmelsbach M, Schlokat U;  
XX WPI; 1998-481211/41.  
XX New factor X analogues with processing site for protease not active  
XX on natural protein - and related DNA, is very stable and can be  
XX activated in vitro or in vivo without using animal protease(s),  
XX particularly for treating disorders of blood coagulation  
XX Claim 4; Page -: 86pp; German.

XX This sequence represents a human Factor X protein analogue which has a  
XX modification that creates a processing site for a protease in the region

CC of the natural F10a activation cleavage site. Such analogues are used to  
CC generate, in vivo or in vitro, F10a analogues that can be used to control  
CC bleeding and for treating defects of factors IX, VII or VIII, e.g. in  
CC haemophiliacs who have developed antibodies to factors VIII and/or IX.  
CC The encoding nucleic acid can be used in gene therapy of the same  
CC conditions. The analogues have high stability and can be activated  
CC without use of animal enzymes such as trypsin. Only activation is  
CC affected, their activity is the same as the natural factor. The analogues  
CC can be isolated as a pure single-chain pro-protein (not usually possible  
CC because of rapid processing of the native precursor) and this converted  
CC to two-chain form by subsequent activation. Activated analogues have good  
CC stability and structural integrity and are practically free of inactive  
CC intermediates and autolytic decomposition products.  
CC NOTE: This sequence does not appear in the specification but has been  
CC constructed from the wild type Factor X protein represented in Figure 1  
CC of the specification.  
XX  
XX SQ Sequence 488 AA;

Query Match 98.6%; Score 2598; DB 19; Length 488;  
Best Local Similarity 98.8%; Pred. No. 2.8e-170;  
Matches 482; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLEEMKKGHLRECEMEE 60  
DB 1 MGRPLHLVLLSASLAGLLLGESLFIIRREQANNILARVTRANSFLEEMKKGHLRECEMEE 60  
QY 61 TCSYEAREVFEFDSKTNFENKYGKDGOCETSPQNGKCKDGIGETCTCLEGFEKGN 120  
DB 61 TCSYEAREVFEFDSKTNFENKYGKDGOCETSPQNGKCKDGIGETCTCLEGFEKGN 120  
QY 121 CELFTRKLCSLONGDCQDFCHEEQNSVVCSCARGVTLADNGKACIPTGPGCKOTLERR 180  
DB 121 CELFTRKLCSLONGDCQDFCHEEQNSVVCSCARGVTLADNGKACIPTGPGCKOTLERR 180  
QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLVIGQEE 240  
DB 181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLVIGQEE 240  
QY 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEEGE 300  
DB 241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAHCLYQAKRFKRVGDRNTEQEEGE 300  
QY 301 AVHEVEVVIKHNRTKETDYDFDIARLKTPTIFRMNVAPACLPDRMAESTLMTQKTI 360  
DB 301 AVHEVEVVIKHNRTKETDYDFDIARLKTPTIFRMNVAPACLPDRMAESTLMTQKTI 360  
QY 361 VSGFGRTHEKGRQSTRKLMLEVPYVDRNSCKLSSEFIITQNMFCAGYDTKQEDACQDGS 420  
DB 361 VSGFGRTHEKGRQSTRKLMLEVPYVDRNSCKLSSEFIITQNMFCAGYDTKQEDACQDGS 420  
QY 421 GPHVTRFDYFTVTVGIVSGWSCARKGKGIYTKVTAFLKWLDRSMKTRGLPKAKSHAPE 480  
DB 421 GPHVTRFDYFTVTVGIVSGWSCARKGKGIYTKVTAFLKWLDRSMKTRGLPKAKSHAPE 480  
QY 481 VITSSPLK 488  
DB 481 VITSSPLK 488

RESULT 8  
AAW40283  
ID AAW40283 standard; Protein; 467 AA.  
XX  
XX AC AAW40283;  
XX DT 16-JUN-1998 (first entry)  
XX DE Human Factor X protease.  
XX  
XX Factor X; factor IX; serine protease activity; catalytic domain; 2AD;  
XX KW zymogen-activating domain; epidermal growth factor-like domain; EGF1;  
XX EGF2; regulator; coagulation; fibrinolysis; homeostasis; X-ray structure;

181	KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNOTQPERGDNNLTRIVGGQE	240
181	KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFLLDFNOTQPERGDNNLTRIVGGQE	240
241	CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVVGRDRNTEQEGGE	300
241	CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVVGRDRNTEQEGGE	300
301	AVHEVEVVIKHNRFETKETYDFDIATVLRKLTPIIFRNMVAPACLPERDWAESTLMTQKTGI	360
301	AVHEVEVVIKHNRFETKETYDFDIATVLRKLTPIIFRNMVAPACLPERDWAESTLMTQKTGI	360
361	VSGFGRTHKRGOSTRLKMLEVYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQDSG	420
361	VSGFGRTHKRGOSTRLKMLEVYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACQDSG	420
421	GPHVTRKDYFYVTGIVSWGECARCKGYGIYTKVTAFLKWLIDRSMTKRLPKAKSHAPE	480
421	GPHVTRKDYFYVTGIVSWGECARCKGYGIYTKVTAFLKWLIDRSMTKRLPKAKSHAPE	480
481	VITSPLK 488	
481	VITSPLK 488	
RESULT 6		
AAW76219	standard; Protein; 488 AA.	
XX	AAW76219;	
XX	27-NOV-1998 (first entry)	
XX	Human Factor X protein analogue.	
DE	Factor X; analogue; activation cleavage site; protease; bleeding; human;	
XX	Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy.	
KW	Homosapiens.	
KW	Synthetic.	
OS	Key	Location/Qualifiers
FF	Peptide	1..40
FT	Protein	/label= signal
FT	Misc-difference 174	41..488
FT	/label= R6	/label= Factor_X
FT	/note= "can be residues Asp, Phe, Thr, Arg, Leu or Ser"	
FT	Misc-difference 175	/label= R5
FT	/note= "can be residues Asn, Lys, Ser, Glu, Gln, Ala, His or Arg"	
FT	Misc-difference 176	/label= R4
FT	/note= "can be residues Thr, Asp, Asn, Ile, Ser, Met, Pro, Arg or Lys"	
FT	Misc-difference 177	/label= R3
FT	/note= "can be residues Leu, Phe, Lys, Met, Gln, Glu, Ser, Val, Arg or Pro"	
FT	Misc-difference 178	/label= R2
FT	/note= "can be residues Glu, Thr, Pro, Gly, Lys or Arg"	
FT	Misc-difference 235	/label= R1
FT	/note= "can be residues Val, Ser, Thr, Ile or Ala"	
XX	W0988318-Al.	
PN	03-SEP-1998.	
XX		
XX		

XX 04-SEP-1990; 90US-0578646.  
 XX (CORT-) COR THERAPEUTICS IN.  
 XX Wolf D;  
 XX WPI; 1992-114303/14.

XX New analogues of Factor Xa peptide - useful for treating  
 PT haemophilia, thrombosis, inflammation and transplant  
 PT complications, for in-vivo diagnosis

XX Claim 3; Fig 1; 59pp; English.

XX The full length cDNA for factor X (see Leytus, S.P. et al., Proc.  
 CC Natl. Acad. Sci. USA (1984) 81: 3699) was subcloned in M13mp19 and  
 CC subjected to site specific mutagenesis to replace Ser 185 and Asp 88.  
 CC In a typical case mutagenesis was first performed with an  
 CC oligonucleotide extending Arg 142 of the light chain by Arg and Lys,  
 CC then aligning with Ile 53 of the activation peptide. When expressed  
 CC in CHO cells the truncated peptide was cleaved endogenously.  
 CC Modified Factor Xa was further produced by acylation e.g. with the  
 CC p-nitrophenyl ester of p-toluoylic acid. Factor Xa is used to  
 CC treat or prevent thrombosis; inflammation; resenosis or complications  
 CC of transplantation. It is also used in treatment of adult respiratory  
 CC distress syndrome and haemophilia. The modified Factor Xa has no  
 CC proteolytic activity and interferes with the ability of endogenous  
 CC factor Xa to convert prothrombin to thrombin. Antibodies reactive  
 CC with Factor Xa are passive therapeutic agents and used for diagnosis.  
 CC See also AAR22513.

XX Sequence 488 AA;

Query Match 99.8%; Score 2630; DB 13; Length 488;  
 Best Local Similarity 99.8%; Pred. No. 1.8e-172;  
 Matches 487; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGRPLHLVLLSASLAGLLLGESLFTIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
 DB 1 MGRPLHLVLLSASLAGLLLGESLFTIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
 QY 61 TCSYEAREVEFSDKTNFENWYKDGQDQETSPCQNGKCKDGLGEYTCCLGEGFEGKN 120  
 DB 61 TCSYEAREVEFSDKTNFENWYKDGQDQETSPCQNGKCKDGLGEYTCCLGEGFEGKN 120  
 QY 121 CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPPCGKQTLERR 180  
 DB 121 CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPPCGKQTLERR 180  
 QY 181 KRSVAQATSSSGEAPDSITWKPYYDAADLDPTENPDLDPNQTPQPERGNNLTRIVGGQE 240  
 DB 181 KRSVAQATSSSGEAPDSITWKPYYDAADLDPTENPDLDPNQTPQPERGNNLTRIVGGQE 240  
 QY 241 CKDGECPWQALLINEEGFCGCTILSEFVILTAHCLYQAKRFKRVGRDNTQEEGGE 300  
 DB 241 CKDGECPWQALLINEEGFCGCTILSEFVILTAHCLYQAKRFKRVGRDNTQEEGGE 300  
 QY 301 AVHEVEVVIKHNFTKTDYDFDIAVLRLKPTITFRMNVAPACLPDRDWAESTILMTQGTGI 360  
 DB 301 AVHEVEVVIKHNFTKTDYDFDIAVLRLKPTITFRMNVAPACLPDRDWAESTILMTQGTGI 360  
 QY 361 VSGFGRTHKGROSTRKMLEVPYDNRNSCKLSSSFIITQNMFCAGYDQKQDAGQDSG 420  
 DB 361 VSGFGRTHKGROSTRKMLEVPYDNRNSCKLSSSFIITQNMFCAGYDQKQDAGQDSG 420  
 QY 421 GPHVTRFKDITYFTVIGSVGEGCARKGKGIYTKVTAFLKWIADRSMTKGLPKAKSHAPE 480  
 DB 421 GPHVTRFKDITYFTVIGSVGEGCARKGKGIYTKVTAFLKWIADRSMTKGLPKAKSHAPE 480  
 QY 481 VITSSPLK 488  
 DB 481 VITSSPLK 488

RESULT 5  
 AAR22512

ID AAR22512 standard; Protein; 488 AA.

AC AAR22512;

DT 28-JUL-1992 (first entry)

DE Mutated precursor of human Factor X analogue.

XX Mutant; prothrombinase complex; proteolytic; precursor; thrombosis;  
 KW inflammation; restenosis; transplantation; haemophilia; antibodies.

OS Homo sapiens.

PN W09204378-A.

PD 19-MAR-1992.

PF 04-SEP-1991; 91WO-US06337.

PR 04-SEP-1990; 90US-0578646.

XX (CORT-) COR THERAPEUTICS IN.

XX Wolf D;

XX WPI; 1992-114303/14.

XX New analogues of Factor Xa peptide - useful for treating  
 PT haemophilia, thrombosis, inflammation and transplant  
 PT complications, for in-vivo diagnosis

XX Claim 3; Fig 1; 59pp; English.

XX The full length cDNA of human factor X was obt'd. from Dr. W.R.  
 CC Church, University of Vermont. This human Factor X cDNA was cloned  
 CC into the EcoRI site of vector pBSII (Stratagene) to obtain pBSX.  
 CC The HindIII-XbaI fragment of pBSX comprising the entire Factor X  
 CC coding region was subcloned into the HindIII-XbaI site of vector  
 CC M13mp19 (Mpi19X). Oligonucleotide site-directed mutagenesis was  
 CC then performed using oligomers to convert serine 185 on the Factor  
 CC X heavy chain to alanine, and to convert aspartic acid 88 on the  
 CC Factor X heavy chain to asparagine. Modified Factor Xa was further  
 CC produced by acylation e.g. with the p-nitrophenyl ester of p-toluoylic  
 CC acid. Modified Factor X is used to treat or prevent thrombosis;  
 CC inflammation; restenosis or complications of transplantation. It  
 CC is also used in treatment of adult respiratory distress syndrome  
 CC and haemophilia. The modified Factor X has no proteolytic activity  
 CC and interferes with the ability of endogenous factor Xa to convert  
 CC prothrombin to thrombin. Antibodies reactive with modified Factor X  
 CC are passive therapeutic agents and used for diagnosis.  
 CC See also AAR22513.

XX Sequence 488 AA;

Query Match 99.5%; Score 2622; DB 13; Length 488;  
 Best Local Similarity 99.4%; Pred. No. 6.4e-172;  
 Matches 485; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGRPLHLVLLSASLAGLLLGESLFTIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
 DB 1 MGRPLHLVLLSASLAGLLLGESLFTIRREQANNILARVTRANSFLEEMKKGHLERECMEE 60  
 QY 61 TCSYEAREVEFSDKTNFENWYKDGQDQETSPCQNGKCKDGLGEYTCCLGEGFEGKN 120  
 DB 61 TCSYEAREVEFSDKTNFENWYKDGQDQETSPCQNGKCKDGLGEYTCCLGEGFEGKN 120  
 QY 121 CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPPCGKQTLERR 180  
 DB 121 CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPPCGKQTLERR 180

QY	61	TCSYEAREVFEDSDKTNEFWNKYKDGOCETSPCQNOGKCKDGLGEYTCCTCLEGEGKN	120
DB	61	TCSYEAREVFEDSDKTNEFWNKYKDGOCETSPCQNOGKCKDGLGEYTCCTCLEGEGKN	120
QY	121	CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR	180
DB	121	CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR	180
QY	181	KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLRIVGGOE	240
DB	181	KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLRIVGGOE	240
QY	241	CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVVGRDRNTEQEGGE	300
DB	241	CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVVGRDRNTEQEGGE	300
QY	301	AVHEVEVVIKHNRTKETDYDFDIIVLRKLTPTITFRMNVAPACILPERDWAESTLMTQKGI	360
DB	301	AVHEVEVVIKHNRTKETDYDFDIIVLRKLTPTITFRMNVAPACILPERDWAESTLMTQKGI	360
QY	361	VSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS	420
DB	361	VSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS	420
QY	421	GPHTVTRFKDYFYVTGIVSWGESCARKGYIYTKVTAFLKWIDRSMTKTRGLPKAKSHAPE	480
DB	421	GPHTVTRFKDYFYVTGIVSWGESCARKGYIYTKVTAFLKWIDRSMTKTRGLPKAKSHAPE	480
QY	481	VITSSPLK 488	
DB	481	VITSSPLK 488	
RESULT 3			
QY	AA70411	411 standard; Protein; 488 AA.	
DB	AA70411	411 standard; Protein; 488 AA.	
QY	02-MY-2001	(first entry)	
DB	02-MY-2001	(first entry)	
QY	Human	factor X protein sequence SEQ ID NO:2.	
DB	Human	factor X; mutant; haemostatic; gene therapy; haemophilia;	
QY	Human	blood coagulation disorder; haemophiliac.	
DB	Human	sapiens.	
QY	WO20110896-A2		
DB	15-FEB-2001.		
QY	07-AUG-2000;	2000WO-EP07631.	
DB	10-AUG-1999;	99AT-0001377.	
QY	(BAXTER )	BAXTER AG.	
DB	Himmelsbach M, Schlokat U;		
QY	WPI; 2001-191516/19.		
DB	N-PS08B; AAF59409.		
QY	Novel	factor X analog useful for producing drug which is useful for	
DB	Novel	treatment of blood coagulation disorders, such as hemophilia, contains	
QY	Novel	modification between amino acids Glu226 and Ile235	
DB	Novel	Disclosure; Fig 1; 50pp; English.	
QY	The	present invention describes a factor X analogue (I) which contains	
DB	The	a modification between Glu226 and Ile235, relative to the 488 residue	
QY	The	amino acid sequence given in AAB70411. (I) has haemostatic activity and	
DB	The	can be used in gene therapy. (I) encoding polynucleotide (II) can be	

CC	used to produce a drug, which is useful for treatment of patients with		
CC	blood coagulation disorders, such as patients suffering from haemophilia,		
CC	or haemophiliacs with inhibitory antibodies. Preparations containing a		
CC	polypeptide with factor X/Xa activity are more readily activated by		
CC	factor Xla or its derivative, which has high stability, without having		
CC	to use one of the proteases used in prior art to activate the natural		
CC	factor X, particularly one of animal origins, such as Russell's viper		
CC	venom (RVV) or trypsin. The present sequence represents human factor X,		
CC	which is given in the exemplification of the present invention.		
XX			
QY	Sequence 488 AA;		
DB	Sequence 488 AA;		
QY	Query Match		
DB	Best Local Similarity 100.0%; Score 2634; DB 22; Length 488;		
QY	Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MGRPLHLVLLSASLAGILLGSLFIRREQANNILARVTRANSFLEEMKKHLEKCEMEE 60		
DB	1 MGRPLHLVLLSASLAGILLGSLFIRREQANNILARVTRANSFLEEMKKHLEKCEMEE 60		
QY	61 TCSYEAREVFEDSDKTNEFWNKYKDGOCETSPCQNOGKCKDGLGEYTCCTCLEGEGKN 120		
DB	61 TCSYEAREVFEDSDKTNEFWNKYKDGOCETSPCQNOGKCKDGLGEYTCCTCLEGEGKN 120		
QY	121 CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180		
DB	121 CELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGYPGCKQTLERR 180		
QY	181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLRIVGGOE 240		
DB	181 KRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNTLRIVGGOE 240		
QY	241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVVGRDRNTEQEGGE 300		
DB	241 CKDGECPWQALLINEENEGFCGGTILSEFYILTAACHLYQAKRFKRVVGRDRNTEQEGGE 300		
QY	301 AVHEVEVVIKHNRTKETDYDFDIIVLRKLTPTITFRMNVAPACILPERDWAESTLMTQKGI 360		
DB	301 AVHEVEVVIKHNRTKETDYDFDIIVLRKLTPTITFRMNVAPACILPERDWAESTLMTQKGI 360		
QY	361 VSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 420		
DB	361 VSGFGRTHKGRQSTRKLMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQDGS 420		
QY	421 GPHTVTRFKDYFYVTGIVSWGESCARKGYIYTKVTAFLKWIDRSMTKTRGLPKAKSHAPE 480		
DB	421 GPHTVTRFKDYFYVTGIVSWGESCARKGYIYTKVTAFLKWIDRSMTKTRGLPKAKSHAPE 480		
QY	481 VITSSPLK 488		
DB	481 VITSSPLK 488		
RESULT 4		AAR22511 standard; Protein; 488 AA.	
QY	AA22511	standard; Protein; 488 AA.	
DB	AA22511	standard; Protein; 488 AA.	
QY	28-JUL-1992	(first entry)	
DB	28-JUL-1992	(first entry)	
QY	Human Factor Xai.		
DB	Human Factor Xai.		
QY	Mutant;	prothrombinase complex; proteolytic; precursor; thrombosis;	
DB	Mutant;	inflammation; restenosis; transplantation; haemophilia; antibodies.	
QY	Homo sapiens.		
DB	Homo sapiens.		
QY	WO9204378-A.		
DB	19-MAR-1992.		
QY	04-SEP-1991;	91WO-US06337.	
DB	04-SEP-1991;	91WO-US06337.	



XX WPI: 1998-481211/41.  
 DR N-PSDB; AAV56776.  
 XX  
 PT New factor X analogues with processing site for protease not active  
 PT on natural protein - and related DNA, is very stable and can be  
 PT activated in vitro or in vivo without using animal protease(s),  
 PT particularly for treating disorders of blood coagulation  
 XX  
 PS Claim 3; Fig 1; 86pp; German.  
 XX  
 CC This sequence represents the human Factor X protein which is used in a  
 CC method resulting in the production of novel human Factor X (F10)  
 CC analogues. Such analogues have in the region of the natural F10a  
 CC activation cleavage site, a modification that creates a processing site  
 CC for a protease that does not naturally cleave F10 in this region. The  
 CC proteins are used to generate, in vivo or in vitro, F10a analogues that  
 CC can be used to control bleeding and for treating defects of factors IX,  
 CC VII or VIII, e.g. in haemophiliacs who have developed antibodies to  
 CC factors VIII and/or IX. The encoding nucleic acid can be used in gene  
 CC therapy of the same conditions. The analogues have high stability and can  
 CC be activated without use of animal enzymes such as trypsin. Only  
 CC activation is affected, their activity is the same as the natural factor.  
 CC The analogues can be isolated as a pure single-chain pro-protein (not  
 CC usually possible because of rapid processing of the native precursor) and  
 CC this converted to two-chain form by subsequent activation. Activated  
 CC analogues have good stability and structural integrity and are  
 CC practically free of inactive intermediates and autoprotoleolytic  
 CC decomposition products.  
 XX  
 SQ Sequence 488 AA;

Query Match 100.0%; Score 2634; DB 19; Length 488;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-173;  
 Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGRPLHLVLLSASLAGLLLGESLFIIRQANNILARVTRANSFLEEMKKGHLERECMEE 60  
 DB 1 MGRPLHLVLLSASLAGLLLGESLFIIRQANNILARVTRANSFLEEMKKGHLERECMEE 60  
 QY 61 TCSYEAREVFEDSDKTNEFWNKYKDGQDQETSPQNGKCKDGLGEYTCCTLEGEFGKN 120  
 DB 61 TCSYEAREVFEDSDKTNEFWNKYKDGQDQETSPQNGKCKDGLGEYTCCTLEGEFGKN 120  
 QY 121 CELFTRKLSLDNGDCDFCHHEQNSVVCSCARGYTLADNGKACIPPGYPCGKQTLERR 180  
 DB 121 CELFTRKLSLDNGDCDFCHHEQNSVVCSCARGYTLADNGKACIPPGYPCGKQTLERR 180  
 QY 181 KRSVAQATSSSGEAPDSITWKPYDAADLPTENPFDLLDFNQTQPERGNNLFRIVGGQE 240  
 DB 181 KRSVAQATSSSGEAPDSITWKPYDAADLPTENPFDLLDFNQTQPERGNNLFRIVGGQE 240  
 QY 241 CKDGECPWQALLINEEGFCGGTILSEFYILTAACHLYQAKRFKVRVGRDNTPEQEGGE 300  
 DB 241 CKDGECPWQALLINEEGFCGGTILSEFYILTAACHLYQAKRFKVRVGRDNTPEQEGGE 300  
 QY 301 AVHEVEVVIKHNRTKETDYDFDIAVLRLKPTIFRNVAPACLPERDWAESTLMTOKTGI 360  
 DB 301 AVHEVEVVIKHNRTKETDYDFDIAVLRLKPTIFRNVAPACLPERDWAESTLMTOKTGI 360  
 QY 361 VSGFGRTHKGRSTRKLMLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACOGDSG 420  
 DB 361 VSGFGRTHKGRSTRKLMLEVPYVDNRNSCKLSSSFIITQNMFCAGYDTKQEDACOGDSG 420  
 QY 421 GPHVTRPKDYFTVTVISWGESCARGKGYIYKVTAFKWDIRSMKTRGLPKAKSHAPE 480  
 DB 421 GPHVTRPKDYFTVTVISWGESCARGKGYIYKVTAFKWDIRSMKTRGLPKAKSHAPE 480  
 QY 481 VITSSPLK 488  
 DB 481 VITSSPLK 488

RESULT 2  
 AAW76218  
 XX AAW76218 standard; Protein; 488 AA.  
 AC AAW76218;  
 XX 27-NOV-1998 (first entry)  
 DT Human Factor X protein.  
 XX  
 DE Factor X; analogue; activation cleavage site; protease; bleeding; human;  
 KW Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FT Peptide 1..40  
 FT Protein /label= signal  
 FT 41..488  
 FT /label= Factor\_X  
 XX W09838318-A1.  
 XX 03-SEP-1998.  
 XX 27-FEB-1998; 98WO-AT00046.  
 XX 27-FEB-1997; 97AT-0000336.  
 XX (IMMO ) IMMUNO AG.  
 XX Dorner F, Eibl J, Falkner F, Himmelsbach M, Pfeleiderer M;  
 PI Schlokat U;  
 XX WPI: 1998-481212/41.  
 DR N-PSDB; AAV56821.  
 XX  
 PT New factor 10 deletion mutants lacking the natural protease  
 PT processing site - but having a non-natural site inserted, and  
 PT related DNA, particularly for in vitro activation to products used  
 PT to treat blood coagulation disorders  
 XX  
 PS Claim 3; Fig 1; 82pp; German.  
 XX  
 CC This sequence represents the human Factor X protein which is used in a  
 CC method resulting in the production of novel human Factor X (F10)  
 CC analogues. Such analogues have in the region of the natural F10a  
 CC activation cleavage site, a modification that creates a processing site  
 CC for a protease that does not naturally cleave F10 in this region. The  
 CC proteins are used to generate, in vivo or in vitro, F10a analogues that  
 CC can be used to control bleeding and for treating defects of factors IX,  
 CC VII or VIII, e.g. in haemophiliacs who have developed antibodies to  
 CC factors VIII and/or IX. The encoding nucleic acid can be used in gene  
 CC therapy of the same conditions. The analogues have high stability and can  
 CC be activated without use of animal enzymes such as trypsin. Only  
 CC activation is affected, their activity is the same as the natural factor.  
 CC The analogues can be isolated as a pure single-chain pro-protein (not  
 CC usually possible because of rapid processing of the native precursor) and  
 CC this converted to two-chain form by subsequent activation. Activated  
 CC analogues have good stability and structural integrity and are  
 CC practically free of inactive intermediates and autoprotoleolytic  
 CC decomposition products.  
 XX  
 SQ Sequence 488 AA;

Query Match 100.0%; Score 2634; DB 19; Length 488;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-173;  
 Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGRPLHLVLLSASLAGLLLGESLFIIRQANNILARVTRANSFLEEMKKGHLERECMEE 60  
 DB 1 MGRPLHLVLLSASLAGLLLGESLFIIRQANNILARVTRANSFLEEMKKGHLERECMEE 60

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2003, 10:16:19 ; Search time 83 seconds  
(without alignments)  
933.236 Million cell updates/sec

Title: US-09-632-722-2

Perfect score: 2634

Sequence: 1 MGRPLHLVLLSASLAGLLLL.....RGLPKAKSHAPVITSSPLK 488

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum D seq length: 0

Maximum D seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2634	100.0	488	19 AAW76216	Human Factor X pro
2	2634	100.0	488	19 AAW76218	Human Factor X pro
3	2634	100.0	488	22 AAB70411	Human factor X pro
4	2630	99.8	488	13 AAR22511	Human Factor xai.
5	2622	99.5	488	13 AAR22512	Mutated precursor
6	2601	98.7	488	19 AAW76219	Human Factor X pro
7	2598	98.6	488	19 AAW76217	Human Factor X pro
8	2605.5	95.1	467	19 AAW40283	Human Factor X pro
9	2441	92.7	448	14 AAR35762	Factor X (X). Hom

10	2436	92.5	448	19 AAW66092	Human factor X var
11	2413	91.6	448	14 AAR37402	Factor X. Homo sa
12	2317	88.0	436	13 AAR22513	Truncated precursor
13	2217.5	84.2	437	17 AAR88468	Human two chain fa
14	1874.5	71.2	509	22 AAB31373	Amino acid sequenc
15	1874.5	71.2	597	22 AAB31374	Amino acid sequenc
16	1851	70.3	492	15 AAR60502	Serine protease fo
17	1847	70.1	487	15 AAR60518	Cattle Factor-Xa.
18	1631	61.9	306	17 AAW05820	Factor X heavy cha
19	1354	51.4	254	17 AAR95597	Factor Xa a form h
20	1289	48.9	241	17 AAR95598	Factor Xa beta for
21	1081	41.0	461	10 AAR93714	Hybrid protein of
22	1051.5	39.9	461	11 AAR05393	Mutant human facto
23	1043	39.6	462	12 AAR10868	Recombinant human
24	1041.5	39.5	456	5 AAP40178	Part of the sequen
25	1041.5	39.5	461	22 AAE10828	Human wild-type fa
26	1041.5	39.5	461	22 AAB60281	Human factor IX (h
27	1041.5	39.5	461	23 AAM05058	Human Factor IX.
28	1039.5	39.5	454	16 AAR67710	Human Factor-IX.
29	1039.5	39.5	461	6 AAP50311	Sequence of human
30	1039.5	39.5	461	6 AAP50302	Sequence of human
31	1039.5	39.5	461	21 AAY97295	Human clotting fac
32	1039.5	39.5	461	23 ABB81908	Protein relating t
33	1039.5	39.5	461	24 ABB95529	Amino acid sequenc
34	1036.5	39.4	456	5. AAB40222	Sequence encoded b
35	1034.5	39.3	461	19 AAW40284	Human Factor IX pr
36	1028.5	39.0	461	6 AAP50019	Sequence of human
37	1021.5	38.8	461	23 AAO21524	Protein of human f
38	996.5	37.8	415	20 AAY03203	Amino acid sequenc
39	992.5	37.7	415	14 AAR35761	Factor IX (IX). H
40	971.5	36.9	412	16 AAR64266	Human Factor-IX.
41	953	36.2	444	16 AAR64205	Factor VII - modif
42	952	36.2	444	22 AAB61992	Human Factor VII p
43	952	36.1	444	21 AAY67967	Factor VII SEQ ID
44	950	36.1	444	19 AAW31687	Homo sapiens Ser34
45	948	36.0	466	7 AAP60056	Factor VII peptide

#### ALIGNMENTS

RESULT 1  
AAW76216  
ID AAW76216 standard; Protein; 488 AA.

XX AC AAW76216;

DT 27-NOV-1998 (first entry)

XX Human Factor X protein.

DE Human Factor X protein.

XX Factor X; analogue; activation cleavage site; protease; bleeding; human;

KW Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..40

FT Protein /label= signal

FT /label= Factor\_X

XX WO9838317-A1.

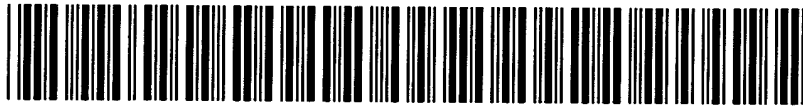
XX 03-SEP-1998.

XX 27-FEB-1998; 98WO-AT00045.

XX 27-FEB-1997; 97AT-0000335.

XX (IMMO ) IMMUNO AG.

XX Dorner F, Eibl J, Fisch A, Himmelspach M, Schlokot U;



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No.	Dccode	Number of pages
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